

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
17 May 2001 (17.05.2001)

PCT

(10) International Publication Number
WO 01/34802 A2

(51) International Patent Classification⁷: C12N 15/12,
15/62, 15/11, 1/21, 5/10, C07K 14/47, 16/18, 19/00, A61K
38/17, 31/70, 39/395, 48/00, G01N 33/68, C12Q 1/68

(21) International Application Number: PCT/US00/30904

(22) International Filing Date:
9 November 2000 (09.11.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
09/439,313 12 November 1999 (12.11.1999) US
09/443,686 18 November 1999 (18.11.1999) US

(71) Applicant (for all designated States except US): CORIXA
CORPORATION [US/US]; Suite 200, 1124 Columbia
Street, Seattle, WA 98104 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): XU, Jiangchun
[US/US]; 15805 SE 43rd Place, Bellevue, WA 98006

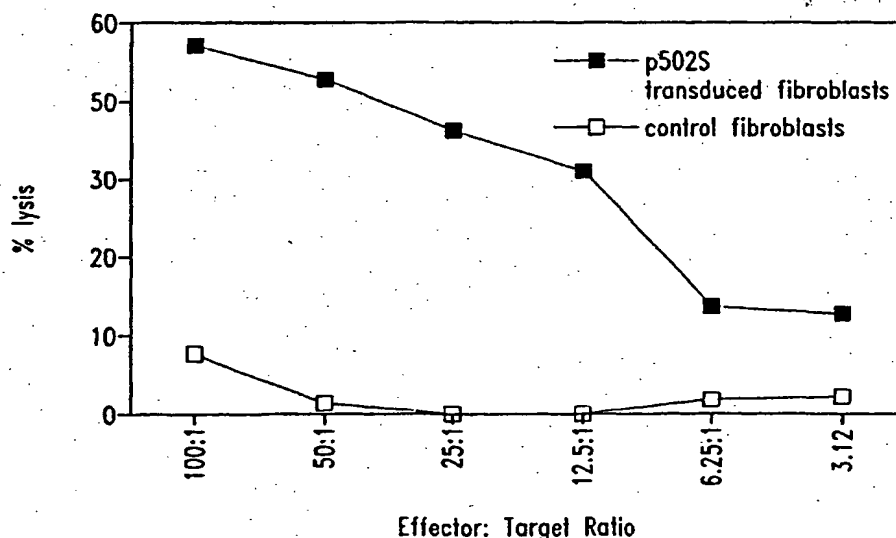
(US). DILLON, Davin, C. [US/US]; 18112 NW Mon-
treux Drive, Issaquah, WA 98027 (US). MITCHAM,
Jennifer, L. [US/US]; 16677 NE 88th Street, Redmond,
WA 98052 (US). HARLOCKER, Susan, L. [US/US];
7522 - 13th Avenue W., Seattle, WA 98117 (US). JIANG,
Yugu [CN/US]; 5001 South 232nd Street, Kent, WA
98032 (US). REED, Steven, G. [US/US]; 2843 - 122nd
Place NE, Bellevue, WA 98005 (US). KALOS, Michael,
D. [US/US]; 8116 Dayton Ave. N., Seattle, WA 98103
(US). RETTER, Marc, W. [US/US]; 33402 NE 43rd
Place, Carnation, WA 98014 (US). STOLK, John, A.
[US/US]; 7436 Northeast 144th Place, Bothell, WA 98011
(US). DAY, Craig, H. [US/US]; 11501 Stone Ave. N.,
C122, Seattle, WA 98133-8317 (US). SKEIKY, Yasir,
A.W. [CA/US]; 15106 SE 47th Place, Bellevue, WA 98006
(US). WANG, Aijun [CN/US]; 3106 213th Place SE,
Issaquah, WA 98029 (US).

(74) Agents: POTTER, Jane, E., R.; Seed Intellectual Prop-
erty Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seat-
tle, WA 98104-7092 et al. (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate-specific proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate-specific protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate-specific protein, or mRNA encoding such a protein, in a sample are also provided.



DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

- (84) Designated States (regional): ARIPO patent (GH, GM, KI, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,

IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— Without international search report and to be republished upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

5 TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate-specific protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for
10 prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress
15 inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but
20 these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate
25 with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

30 SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the

diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a prostate-specific protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate-specific protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-550.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate-specific protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines for prophylactic or therapeutic use are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and an immunostimulant.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate-specific protein; and (b) a physiologically acceptable carrier. In certain embodiments, the present invention provides monoclonal antibodies that specifically bind to an amino acid sequence selected from the group consisting of SEQ ID NO: 496, 504, 505, 509-517, 522 and 541-550, together with monoclonal antibodies comprising a complementarity determining region selected from the group consisting of SEQ ID NO: 502, 503 and 506-508.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

5 Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

10 Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with an immunostimulant.

15 Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that
20 specifically react with a prostate-specific protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described
25 above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate-specific protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time
30 sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate-specific protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain

embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate-specific polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate-specific polypeptide P502S. In each case, the number of γ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/neu.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

5 Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

10 Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate-specific polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

15 Figures 6A and 6B are graphs illustrating the specificity of a CD8⁺ cell line (3A-1) for a representative prostate-specific antigen (P501S). Figure 6A shows the results of a ⁵¹Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

Figure 7 is a Western blot showing the expression of P501S in baculovirus.

Figure 8 illustrates the results of epitope mapping studies on P501S.

20 Figure 9 is a schematic representation of the P501S protein showing the location of transmembrane domains and predicted intracellular and extracellular domains.

Figure 10 is a genomic map showing the location of the prostate genes P775P, P704P, B305D, P712P and P774P within the Cat Eye Syndrome region of chromosome 22q11.2

25 Figure 11 shows the results of an ELISA assay of antibody specificity to P501S peptides.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16

30 SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1

SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9

SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4

- SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12
5 SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862
SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13
SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19
10 SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19
SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25
SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25
SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24
SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24
15 SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58
SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58
SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63
SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63
SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4
20 SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4
SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16
25 SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21
SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48
SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6
30 SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858
SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

- SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864
- SEQ ID NO: 41 is the determined cDNA sequence for P5
- SEQ ID NO: 42 is the determined cDNA sequence for P8
- SEQ ID NO: 43 is the determined cDNA sequence for P9
- 5 SEQ ID NO: 44 is the determined cDNA sequence for P18
- SEQ ID NO: 45 is the determined cDNA sequence for P20
- SEQ ID NO: 46 is the determined cDNA sequence for P29
- SEQ ID NO: 47 is the determined cDNA sequence for P30
- SEQ ID NO: 48 is the determined cDNA sequence for P34
- 10 SEQ ID NO: 49 is the determined cDNA sequence for P36
- SEQ ID NO: 50 is the determined cDNA sequence for P38
- SEQ ID NO: 51 is the determined cDNA sequence for P39
- SEQ ID NO: 52 is the determined cDNA sequence for P42
- SEQ ID NO: 53 is the determined cDNA sequence for P47
- 15 SEQ ID NO: 54 is the determined cDNA sequence for P49
- SEQ ID NO: 55 is the determined cDNA sequence for P50
- SEQ ID NO: 56 is the determined cDNA sequence for P53
- SEQ ID NO: 57 is the determined cDNA sequence for P55
- SEQ ID NO: 58 is the determined cDNA sequence for P60
- 20 SEQ ID NO: 59 is the determined cDNA sequence for P64
- SEQ ID NO: 60 is the determined cDNA sequence for P65
- SEQ ID NO: 61 is the determined cDNA sequence for P73
- SEQ ID NO: 62 is the determined cDNA sequence for P75
- SEQ ID NO: 63 is the determined cDNA sequence for P76
- 25 SEQ ID NO: 64 is the determined cDNA sequence for P79
- SEQ ID NO: 65 is the determined cDNA sequence for P84
- SEQ ID NO: 66 is the determined cDNA sequence for P68
- SEQ ID NO: 67 is the determined cDNA sequence for P80
- SEQ ID NO: 68 is the determined cDNA sequence for P82
- 30 SEQ ID NO: 69 is the determined cDNA sequence for U1-3064
- SEQ ID NO: 70 is the determined cDNA sequence for U1-3065
- SEQ ID NO: 71 is the determined cDNA sequence for V1-3692

- SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905
SEQ ID NO: 73 is the determined cDNA sequence for V1-3686
SEQ ID NO: 74 is the determined cDNA sequence for R1-2330
SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976
5 SEQ ID NO: 76 is the determined cDNA sequence for V1-3679
SEQ ID NO: 77 is the determined cDNA sequence for 1G-4736
SEQ ID NO: 78 is the determined cDNA sequence for 1G-4738
SEQ ID NO: 79 is the determined cDNA sequence for 1G-4741
SEQ ID NO: 80 is the determined cDNA sequence for 1G-4744
10 SEQ ID NO: 81 is the determined cDNA sequence for 1G-4734
SEQ ID NO: 82 is the determined cDNA sequence for 1H-4774
SEQ ID NO: 83 is the determined cDNA sequence for 1H-4781
SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785
SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787
15 SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796
SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807
SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810
SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811
SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876
20 SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884
SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896
SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761
SEQ ID NO: 94 is the determined cDNA sequence for 1G-4762
SEQ ID NO: 95 is the determined cDNA sequence for 1H-4766
25 SEQ ID NO: 96 is the determined cDNA sequence for 1H-4770
SEQ ID NO: 97 is the determined cDNA sequence for 1H-4771
SEQ ID NO: 98 is the determined cDNA sequence for 1H-4772
SEQ ID NO: 99 is the determined cDNA sequence for 1D-4297
SEQ ID NO: 100 is the determined cDNA sequence for 1D-4309
30 SEQ ID NO: 101 is the determined cDNA sequence for 1D-4278
SEQ ID NO: 102 is the determined cDNA sequence for 1D-4288
SEQ ID NO: 103 is the determined cDNA sequence for 1D-4283

SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304

SEQ ID NO: 105 is the determined cDNA sequence for 1D-4296

SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280

SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12 (also referred to as P504S)

5

SEQ ID NO: 108 is the predicted amino acid sequence for F1-12

SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17

SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862 (also referred to as

10 P503S)

SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

SEQ ID NO: 113 is the predicted amino acid sequence for L1-12 (also referred to as P501S)

SEQ ID NO: 114 is the predicted amino acid sequence for N1-1862 (also referred to as P503S)

SEQ ID NO: 115 is the determined cDNA sequence for P89

15 SEQ ID NO: 116 is the determined cDNA sequence for P90

SEQ ID NO: 117 is the determined cDNA sequence for P92

SEQ ID NO: 118 is the determined cDNA sequence for P95

SEQ ID NO: 119 is the determined cDNA sequence for P98

SEQ ID NO: 120 is the determined cDNA sequence for P102

20 SEQ ID NO: 121 is the determined cDNA sequence for P110

SEQ ID NO: 122 is the determined cDNA sequence for P111

SEQ ID NO: 123 is the determined cDNA sequence for P114

SEQ ID NO: 124 is the determined cDNA sequence for P115

SEQ ID NO: 125 is the determined cDNA sequence for P116

25 SEQ ID NO: 126 is the determined cDNA sequence for P124

SEQ ID NO: 127 is the determined cDNA sequence for P126

SEQ ID NO: 128 is the determined cDNA sequence for P130

SEQ ID NO: 129 is the determined cDNA sequence for P133

SEQ ID NO: 130 is the determined cDNA sequence for P138

30 SEQ ID NO: 131 is the determined cDNA sequence for P143

SEQ ID NO: 132 is the determined cDNA sequence for P151

SEQ ID NO: 133 is the determined cDNA sequence for P156

- SEQ ID NO: 134 is the determined cDNA sequence for P157
SEQ ID NO: 135 is the determined cDNA sequence for P166
SEQ ID NO: 136 is the determined cDNA sequence for P176
SEQ ID NO: 137 is the determined cDNA sequence for P178
5 SEQ ID NO: 138 is the determined cDNA sequence for P179
SEQ ID NO: 139 is the determined cDNA sequence for P185
SEQ ID NO: 140 is the determined cDNA sequence for P192
SEQ ID NO: 141 is the determined cDNA sequence for P201
SEQ ID NO: 142 is the determined cDNA sequence for P204
10 SEQ ID NO: 143 is the determined cDNA sequence for P208
SEQ ID NO: 144 is the determined cDNA sequence for P211
SEQ ID NO: 145 is the determined cDNA sequence for P213
SEQ ID NO: 146 is the determined cDNA sequence for P219
SEQ ID NO: 147 is the determined cDNA sequence for P237
15 SEQ ID NO: 148 is the determined cDNA sequence for P239
SEQ ID NO: 149 is the determined cDNA sequence for P248
SEQ ID NO: 150 is the determined cDNA sequence for P251
SEQ ID NO: 151 is the determined cDNA sequence for P255
SEQ ID NO: 152 is the determined cDNA sequence for P256
20 SEQ ID NO: 153 is the determined cDNA sequence for P259
SEQ ID NO: 154 is the determined cDNA sequence for P260
SEQ ID NO: 155 is the determined cDNA sequence for P263
SEQ ID NO: 156 is the determined cDNA sequence for P264
SEQ ID NO: 157 is the determined cDNA sequence for P266
25 SEQ ID NO: 158 is the determined cDNA sequence for P270
SEQ ID NO: 159 is the determined cDNA sequence for P272
SEQ ID NO: 160 is the determined cDNA sequence for P278
SEQ ID NO: 161 is the determined cDNA sequence for P105
SEQ ID NO: 162 is the determined cDNA sequence for P107
30 SEQ ID NO: 163 is the determined cDNA sequence for P137
SEQ ID NO: 164 is the determined cDNA sequence for P194
SEQ ID NO: 165 is the determined cDNA sequence for P195

- SEQ ID NO: 166 is the determined cDNA sequence for P196
SEQ ID NO: 167 is the determined cDNA sequence for P220
SEQ ID NO: 168 is the determined cDNA sequence for P234
SEQ ID NO: 169 is the determined cDNA sequence for P235
5 SEQ ID NO: 170 is the determined cDNA sequence for P243
SEQ ID NO: 171 is the determined cDNA sequence for P703P-DE1
SEQ ID NO: 172 is the predicted amino acid sequence for P703P-DE1
SEQ ID NO: 173 is the determined cDNA sequence for P703P-DE2
SEQ ID NO: 174 is the determined cDNA sequence for P703P-DE6
10 SEQ ID NO: 175 is the determined cDNA sequence for P703P-DE13
SEQ ID NO: 176 is the predicted amino acid sequence for P703P-DE13
SEQ ID NO: 177 is the determined cDNA sequence for P703P-DE14
SEQ ID NO: 178 is the predicted amino acid sequence for P703P-DE14
SEQ ID NO: 179 is the determined extended cDNA sequence for 1G-4736
15 SEQ ID NO: 180 is the determined extended cDNA sequence for 1G-4738
SEQ ID NO: 181 is the determined extended cDNA sequence for 1G-4741
SEQ ID NO: 182 is the determined extended cDNA sequence for 1G-4744
SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-4774
SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-4781
20 SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-4785
SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-4787
SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-4796
SEQ ID NO: 188 is the determined extended cDNA sequence for 1I-4807
SEQ ID NO: 189 is the determined 3' cDNA sequence for 1I-4810
25 SEQ ID NO: 190 is the determined 3' cDNA sequence for 1I-4811
SEQ ID NO: 191 is the determined extended cDNA sequence for 1J-4876
SEQ ID NO: 192 is the determined extended cDNA sequence for 1K-4884
SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-4896
SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-4761
30 SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-4762
SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-4766
SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770

- SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771
- SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-4772
- SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309
- SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278
- 5 SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288
- SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283
- SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304
- SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296
- SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280
- 10 SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd
- SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con
- SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev
- SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd
- SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev
- 15 SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd
- SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev
- SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd
- SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev
- SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd
- 20 SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev
- SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd
- SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev
- SEQ ID NO: 220 is the determined cDNA sequence for 8-h11 rev
- SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd
- 25 SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev
- SEQ ID NO: 223 is the determined cDNA sequence for P509S
- SEQ ID NO: 224 is the determined cDNA sequence for P510S
- SEQ ID NO: 225 is the determined cDNA sequence for P703DE5
- SEQ ID NO: 226 is the determined cDNA sequence for 9-A11
- 30 SEQ ID NO: 227 is the determined cDNA sequence for 8-C6
- SEQ ID NO: 228 is the determined cDNA sequence for 8-H7
- SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13

- SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23
SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25
5 SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35
SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38
10 SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41
SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42
SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45
15 SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65
20 SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86
25 SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2
30 SEQ ID NO: 259 is the determined cDNA sequence for JP1B1
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3

- SEQ ID NO: 262 is the determined cDNA sequence for JP1A4
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6
5 SEQ ID NO: 266 is the determined cDNA sequence for JP1B5
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9
10 SEQ ID NO: 271 is the determined cDNA sequence for JP1C10
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11
15 SEQ ID NO: 276 is the determined cDNA sequence for JP1C11
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2
20 SEQ ID NO: 281 is the determined cDNA sequence for JP8H1
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3
25 SEQ ID NO: 286 is the determined cDNA sequence for JP8G4
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8
30 SEQ ID NO: 291 is the determined cDNA sequence for JP8C7
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7
SEQ ID NO: 293 is the determined cDNA sequence for P8D8

- SEQ ID NO: 294 is the determined cDNA sequence for JP8E7
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10
5 SEQ ID NO: 298 is the determined cDNA sequence for JP8C10
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9
10 SEQ ID NO: 303 is the determined cDNA sequence for JP8C12
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12
SEQ ID NO: 307 is the determined cDNA sequence for P711P
15 SEQ ID NO: 308 is the determined cDNA sequence for P712P
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23
SEQ ID NO: 310 is the determined cDNA sequence for P774P
SEQ ID NO: 311 is the determined cDNA sequence for P775P
SEQ ID NO: 312 is the determined cDNA sequence for P715P
20 SEQ ID NO: 313 is the determined cDNA sequence for P710P
SEQ ID NO: 314 is the determined cDNA sequence for P767P
SEQ ID NO: 315 is the determined cDNA sequence for P768P
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5
25 SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26
SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23
30 SEQ ID NO: 332 is the determined full length cDNA sequence for P509S
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)
SEQ ID NO: 334 is the determined cDNA sequence for P714P

SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)

SEQ ID NO: 336 is the predicted amino acid sequence for P705P

SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10

SEQ ID NO: 338 is the amino acid sequence of the peptide p5

5 SEQ ID NO: 339 is the predicted amino acid sequence of P509S

SEQ ID NO: 340 is the determined cDNA sequence for P778P

SEQ ID NO: 341 is the determined cDNA sequence for P786P

SEQ ID NO: 342 is the determined cDNA sequence for P789P

10 SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

15 SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

20 SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

25 SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

30 SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

5 SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

10 SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

15 SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

SEQ ID NO: 381 is the determined cDNA sequence for B716P.

SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.

20 SEQ ID NO: 383 is the predicted amino acid sequence for P711P.

SEQ ID NO: 384 is the cDNA sequence for P1000C.

SEQ ID NO: 385 is the cDNA sequence for CGI-82.

SEQ ID NO: 386 is the cDNA sequence for 23320.

SEQ ID NO: 387 is the cDNA sequence for CGI-69.

25 SEQ ID NO: 388 is the cDNA sequence for L-iditol-2-dehydrogenase.

SEQ ID NO: 389 is the cDNA sequence for 23379.

SEQ ID NO: 390 is the cDNA sequence for 23381.

SEQ ID NO: 391 is the cDNA sequence for KIAA0122.

SEQ ID NO: 392 is the cDNA sequence for 23399.

30 SEQ ID NO: 393 is the cDNA sequence for a previously identified gene.

SEQ ID NO: 394 is the cDNA sequence for HCLBP.

SEQ ID NO: 395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

5 SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

10 SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553.

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

15 SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.

20 SEQ ID NO:415 is the cDNA sequence for 22572.

SEQ ID NO:416 is the cDNA sequence for 22573.

SEQ ID NO:417 is the cDNA sequence for 22573.

SEQ ID NO:418 is the cDNA sequence for 22575.

SEQ ID NO:419 is the cDNA sequence for 22580.

25 SEQ ID NO:420 is the cDNA sequence for 22581.

SEQ ID NO:421 is the cDNA sequence for 22582.

SEQ ID NO:422 is the cDNA sequence for 22583.

SEQ ID NO:423 is the cDNA sequence for 22584.

SEQ ID NO:424 is the cDNA sequence for 22585.

30 SEQ ID NO:425 is the cDNA sequence for 22586.

SEQ ID NO:426 is the cDNA sequence for 22587.

SEQ ID NO:427 is the cDNA sequence for 22588.

- SEQ ID NO:428 is the cDNA sequence for 22589.
SEQ ID NO:429 is the cDNA sequence for 22590.
SEQ ID NO:430 is the cDNA sequence for 22591.
SEQ ID NO:431 is the cDNA sequence for 22592.
5 SEQ ID NO:432 is the cDNA sequence for 22593.
SEQ ID NO:433 is the cDNA sequence for 22594.
SEQ ID NO:434 is the cDNA sequence for 22595.
SEQ ID NO:435 is the cDNA sequence for 22596.
SEQ ID NO:436 is the cDNA sequence for 22847.
10 SEQ ID NO:437 is the cDNA sequence for 22848.
SEQ ID NO:438 is the cDNA sequence for 22849.
SEQ ID NO:439 is the cDNA sequence for 22851.
SEQ ID NO:440 is the cDNA sequence for 22852.
SEQ ID NO:441 is the cDNA sequence for 22853.
15 SEQ ID NO:442 is the cDNA sequence for 22854.
SEQ ID NO:443 is the cDNA sequence for 22855.
SEQ ID NO:444 is the cDNA sequence for 22856.
SEQ ID NO:445 is the cDNA sequence for 22857.
SEQ ID NO:446 is the cDNA sequence for 23601.
20 SEQ ID NO:447 is the cDNA sequence for 23602.
SEQ ID NO:448 is the cDNA sequence for 23605.
SEQ ID NO:449 is the cDNA sequence for 23606.
SEQ ID NO:450 is the cDNA sequence for 23612.
SEQ ID NO:451 is the cDNA sequence for 23614.
25 SEQ ID NO:452 is the cDNA sequence for 23618.
SEQ ID NO:453 is the cDNA sequence for 23622.
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.
SEQ ID NO:455 is the cDNA sequence for LIM protein.
SEQ ID NO:456 is the cDNA sequence for a known gene.
30 SEQ ID NO:457 is the cDNA sequence for a known gene.
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.
SEQ ID NO:459 is the cDNA sequence for 23045.

SEQ ID NO:460 is the cDNA sequence for 23032.

SEQ ID NO:461 is the cDNA sequence for 23054.

SEQ ID NO:462-467 are cDNA sequences for known genes.

SEQ ID NO:468-471 are cDNA sequences for P710P.

5 SEQ ID NO:472 is a cDNA sequence for P1001C.

SEQ ID NO: 473 is the determined cDNA sequence for a first splice variant of P775P (referred to as 27505).

SEQ ID NO: 474 is the determined cDNA sequence for a second splice variant of P775P (referred to as 19947).

10 SEQ ID NO: 475 is the determined cDNA sequence for a third splice variant of P775P (referred to as 19941).

SEQ ID NO: 476 is the determined cDNA sequence for a fourth splice variant of P775P (referred to as 19937).

15 SEQ ID NO: 477 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.

SEQ ID NO: 478 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 474.

SEQ ID NO: 479 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 475.

20 SEQ ID NO: 480 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 481 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

25 SEQ ID NO: 482 is a third predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 483 is a fourth predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 484 is the first 30 amino acids of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 485 is the PCR primer AW025.

30 SEQ ID NO: 486 is the PCR primer AW003.

SEQ ID NO: 487 is the PCR primer AW027.

SEQ ID NO: 488 is the PCR primer AW026.

SEQ ID NO: 489-501 are peptides employed in epitope mapping studies.

SEQ ID NO: 502 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody 20D4.

SEQ ID NO: 503 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody JA1.

SEQ ID NO: 504 & 505 are peptides employed in epitope mapping studies.

SEQ ID NO: 506 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 8H2.

SEQ ID NO: 507 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 7H8.

SEQ ID NO: 508 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 2D4.

SEQ ID NO: 509-522 are peptides employed in epitope mapping studies.

SEQ ID NO: 523 is a mature form of P703P used to raise antibodies against P703P. SEQ ID NO:

524 is the putative full-length cDNA sequence of P703P.

SEQ ID NO: 525 is the predicted amino acid sequence encoded by SEQ ID NO: 524.

SEQ ID NO: 526 is the full-length cDNA sequence for P790P.

SEQ ID NO: 527 is the predicted amino acid sequence for P790P.

SEQ ID NO: 528 & 529 are PCR primers.

SEQ ID NO: 530 is the cDNA sequence of a splice variant of SEQ ID NO: 366.

SEQ ID NO: 531 is the cDNA sequence of the open reading frame of SEQ ID NO: 530.

SEQ ID NO: 532 is the predicted amino acid encoded by the sequence of SEQ ID NO: 531.

SEQ ID NO: 533 is the DNA sequence of a putative ORF of P775P.

SEQ ID NO: 534 is the predicted amino acid sequence encoded by SEQ ID NO: 533.

SEQ ID NO: 535 is a first full-length cDNA sequence for P510S.

SEQ ID NO: 536 is a second full-length cDNA sequence for P510S.

SEQ ID NO: 537 is the predicted amino acid sequence encoded by SEQ ID NO: 535.

SEQ ID NO: 538 is the predicted amino acid sequence encoded by SEQ ID NO: 536.

SEQ ID NO: 539 is the peptide P501S-370.

SEQ ID NO: 540 is the peptide P501S-376.

SEQ ID NO: 541-550 are epitopes of P501S.

SEQ ID NO: 551 corresponds to amino acids 543-553 of P501S.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate-specific polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (e.g., T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate-specific protein or a variant thereof. A "prostate-specific protein" is a protein that is expressed in normal prostate and/or prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a non-prostate normal tissue, as determined using a representative assay provided herein. Certain prostate-specific proteins are proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate-specific proteins. Sequences of polynucleotides encoding certain prostate-specific proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536. Sequences of polypeptides comprising at least a portion of a prostate-specific protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534 and 537-550.

PROSTATE-SPECIFIC PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate-specific protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred

polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate-specific protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate-specific protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate-specific protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate-specific protein or a portion thereof. The term "variants" also encompasses homologous genes of xenogenic origin.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices

for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenesis pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate-specific protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such

as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate-specific than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate-specific cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, a prostate-specific cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into

a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (see Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate-specific protein are provided in SEQ ID NO:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536.

Isolation of these polynucleotides is described below. Each of these prostate-specific proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate-specific protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate-specific polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3'

ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-, methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

5 Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector
10 will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for
15 therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). The polynucleotides may also be administered as naked plasmid vectors.
20 Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary
25 skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (i.e., an artificial membrane
30 vesicle). The preparation and use of such systems is well known in the art.

PROSTATE-SPECIFIC POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate-specific protein or a variant thereof, as described herein. As noted above, a "prostate-specific protein" is a protein that is expressed by normal prostate and/or prostate tumor cells. Proteins that are prostate-specific proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate-specific protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate-specific protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the

immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ^{125}I -labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate-specific protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate-specific protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most-preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino

acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, higher eukaryotic and plant cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known prostate-specific protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner),

preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are

located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its

original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector
5 that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate-specific protein. As used herein, an
10 antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate-specific protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate-specific protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding
15 constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

20 Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate-specific protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals
25 without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the
30 above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Most preferably, antibodies employed in the inventive methods have the ability to induce lysis of tumor cells by activation of complement and mediation of antibody-dependent cellular cytotoxicity (ADCC). Antibodies of different classes and subclasses differ in these properties. For example, mouse antibodies of the IgG2a and IgG3 classes are capable of activating serum complement upon binding to target cells which express the antigen against which the antibodies were raised, and can mediate ADCC.

Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells

and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse.

Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

The preparation of mouse and rabbit monoclonal antibodies that specifically bind to polypeptides of the present invention is described in detail below. However, the antibodies of the present invention are not limited to those derived from mice. Human antibodies may also be employed in the inventive methods and may prove to be preferable. Such antibodies can be obtained using human hybridomas as described by Cote *et al.* (Monoclonal Antibodies and Cancer Therapy, Alan R. Lisa, p. 77, 1985). The present invention also encompasses antibodies made by recombinant means such as chimeric antibodies, wherein the variable region and constant region are derived from different species, and CDR-grafted antibodies, wherein the complementarity determining region is derived from a different species, as described in US Patents 4,816,567 and 5,225,539. Chimeric antibodies may be prepared by splicing genes for a mouse antibody molecule having a desired antigen specificity together with genes for a human antibody molecule having the desired biological activity, such as activation of human complement and mediation of ADCC (Morrison *et al. Proc. Natl. Acad. Sci. USA* 81:6851, 1984; Neuberger *et al. Nature* 312:604, 1984; Takeda *et al. Nature* 314:452, 1985).

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*,

Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to

Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

5 It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or
10 linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent
15 No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating
20 compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of
25 a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

30 Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate-specific protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral

blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the ISOLEX™ system, available from Nexell Therapeutics Inc., Irvine, CA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate-specific polypeptide, polynucleotide encoding a prostate-specific polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate-specific polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate-specific polypeptide if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate-specific polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a prostate-specific polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Prostate-specific protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a prostate-specific polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate-specific polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate-specific polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate-specific protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression

in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA

or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example,

an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent
5 adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release
10 formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix
15 and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical
20 compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the
25 antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or
30 progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy,

Ann. Rev. Med. 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take-up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface
5 receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone
10 marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into
15 dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this
20 nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II
25 MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a prostate-specific protein (or portion or other variant thereof) such that the prostate-specific polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex*
30 *vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection

that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the prostate-specific polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer

cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate
5 antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in*
10 *vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte,
15 fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies
20 have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back
25 into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established
30 using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered

over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50%
5 above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-
10 vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active
15 compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate-specific protein generally correlate with an improved clinical outcome. Such immune responses may generally be
20 evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or
25 more prostate-specific proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the
30 agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer.

In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length prostate-specific proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a

membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by

assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains
5 a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of
10 time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and
15 fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a
20 signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is
25 determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest
30 to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along

the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate-specific polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate-specific protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate-specific protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a prostate-specific polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that

expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate-specific polypeptide (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate-specific polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate-specific protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate-specific protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate-specific protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate-specific protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382, 384-476, 524, 526, 530, 531, 533, 535 and 536. Techniques for both PCR based assays and hybridization assays

are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51:263, 1987; Erlich ed., PCR Technology, Stockton Press, NY, 1989*).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate-specific protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for proteins provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate-specific protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate-specific protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate-specific protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate-specific protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as

follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As
5 recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with
10 BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and
15 incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA
20 was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and
25 grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively,
30 with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA

library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show
5 some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid
10 sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided
15 in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating
20 sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in
30 SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated

clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA⁺ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni,

Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339. Two variant full-length cDNA sequences for P510S are provided in SEQ ID NO: 535 and 536, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 537 and 538, respectively.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE-SPECIFIC POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate-specific polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each

reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney,

but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmataz *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of

2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. The putative full-length cDNA sequence for P703P is provided in SEQ ID NO: 524, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 525.

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

Further studies on P775P resulted in the isolation of four additional sequences (SEQ ID NO: 473-476) which are all splice variants of the P775P gene. The sequence of SEQ ID NO: 474 was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 477 and 478. The cDNA sequence of SEQ ID NO: 475 was found to contain an ORF which encodes the amino acid sequence of SEQ ID NO: 479. The cDNA sequence of SEQ ID NO: 473 was found to contain four ORFs. The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 480-483.

Subsequent studies led to the identification of a genomic region on chromosome 22q11.2, known as the Cat Eye Syndrome region, that contains the five prostate genes P704P, P712P, P774P, P775P and B305D. The relative location of each of these five genes within the genomic region is shown in Fig. 10. This region may therefore be associated with malignant tumors, and other potential tumor genes may be contained within this region. These studies also led

to the identification of a potential open reading frame (ORF) for P775P (provided in SEQ ID NO: 533), which encodes the amino acid sequence of SEQ ID NO: 534.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the

subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most

recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350, 351 and 353-365.

Further studies on the clone of SEQ ID NO: 352 (referred to as P790P) led to the isolation of the full-length cDNA sequence of SEQ ID NO: 526. The corresponding predicted amino acid is provided in SEQ ID NO: 527. Data from two quantitative PCR experiments indicated that P790P is over-expressed in 11/15 tested prostate tumor samples and is expressed at low levels in spinal cord, with no expression being seen in all other normal samples tested. Data from further PCR experiments and microarray experiments showed over-expression in normal prostate and prostate tumor with little or no expression in other tissues tested. P790P was subsequently found to show significant homology to a previously identified G-protein coupled prostate tissue receptor.

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

5 6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2Kb (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID
10 NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100µg of P2S#12 and 120µg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6×10^6 cells/ml in complete media (RPMI-1640; Gibco
15 BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2×10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells ($5 \times$
20 10^5 /ml) were restimulated with 2.5×10^6 /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb
25 tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2Kb expressing) transduced with P502S than against control fibroblasts. An example is presented in
30 Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2Kb molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 µg/ml were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2Kb were immunized as described by Theobald *et al*. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5µg of P1S #10 and 120µg of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6×10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2µg/ml P1S#10 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later cells (5×10^5 /ml) were restimulated with 2.5×10^6 /ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate-specific antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 μ g P501S in the vector VR1012 either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed HLA-A2-restricted CTL epitope.

EXAMPLE 8

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE-SPECIFIC POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8⁺ T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8⁺ T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a γ -interferon

ELISPOT assay (see Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10^4 fibroblasts in the presence of 3 $\mu\text{g/ml}$ human β_2 -microglobulin and 1 $\mu\text{g/ml}$ P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml γ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

EXAMPLE 9

ELICITATION OF PROSTATE ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate-specific antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GMCSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8⁺ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles using autologous fibroblasts retrovirally transduced

to express P501S and CD80, CD8+ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (^{51}Cr release) and interferon-gamma production (Interferon-gamma Elispot; see above and Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN A PROSTATE-SPECIFIC ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific human CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed and P703P-transduced target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2Kb transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of HLA-A2Kb or HLA-A2 transduced target cells expressing P703P.

Initial studies demonstrating that p5 is a naturally processed epitope were done using HLA-A2Kb transgenic mice. HLA-A2Kb transgenic mice were immunized subcutaneously in the footpad with 100 μg of p5 peptide together with 140 μg of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived

from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with 1 ug/ml p5 peptide and cultured with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated. CTL were additionally shown to recognize human cells transduced to express P703P, demonstrating that p5 is a naturally processed epitope.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively. In further studies, a splice variant of the cDNA sequence of SEQ ID NO: 366 was isolated which was found to contain an additional guanine residue at position 884 (SEQ ID NO: 530), leading to a frameshift in the open reading frame. The determined DNA sequence of this ORF is provided in SEQ ID NO: 531. This frameshift generates a protein sequence (provided in SEQ ID NO: 532) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach).

EXAMPLE 12

GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH PROSTATE-SPECIFIC ANTIGEN

Using *in vitro* whole-gene priming with P501S-vaccinia infected DC (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon- γ ELISPOT analysis as described above. Using a panel of HLA-mismatched B-LCL lines transduced with P501S, these CTL lines were shown to be likely restricted to HLAB class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 μ g/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S and CD80. Following four stimulation cycles, CD8+ T cell lines were identified that specifically produced interferon- γ when stimulated with P501S and CD80-transduced autologous fibroblasts. A panel of HLA-mismatched B-LCL lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- γ in an ELISPOT assay, the P501S specific response was shown to be likely restricted by HLA B alleles. These results demonstrate that a CD8+ CTL response to P501S can be elicited.

To identify the epitope(s) recognized, cDNA encoding P501S was fragmented by various restriction digests, and sub-cloned into the retroviral expression vector pBIB-KS. Retroviral supernatants were generated by transfection of the helper packaging line Phoenix-Ampho. Supernatants were then used to transduce Jurkat/A2Kb cells for CTL screening. CTL were screened in IFN-gamma ELISPOT assays against these A2Kb targets transduced with the "library" of P501S fragments. Initial positive fragments P501S/H3 and P501S/F2 were sequenced and found to encode amino acids 106-553 and amino acids 136-547, respectively, of SEQ ID NO: 113. A truncation of H3 was made to encode amino acid residues 106-351 of SEQ ID NO: 113, which was unable to stimulate the CTL, thus localizing the epitope to amino acid residues 351-547. Additional fragments encoding amino acids 1-472 (Fragment A) and amino acids 1-351 (Fragment B) were also constructed. Fragment A but not Fragment B stimulated the CTL thus localizing the epitope to amino acid residues 351-472. Overlapping 20-mer and 18-mer peptides representing this region were tested by pulsing Jurkat/A2Kb cells versus CTL in an IFN-gamma assay. Only peptides

P501S-369(20) and P501S-369(18) stimulated the CTL. Nine-mer and 10-mer peptides representing this region were synthesized and similarly tested. Peptide P501S-370 (SEQ ID NO: 539) was the minimal 9-mer giving a strong response. Peptide P501S-376 (SEQ ID NO: 540) also gave a weak response, suggesting that it might represent a cross-reactive epitope.

5 In subsequent studies, the ability of primary human B cells transduced with P501S to prime MHC class I-restricted, P501S-specific, autologous CD8 T cells was examined. Primary B cells were derived from PBMC of a homozygous HLA-A2 donor by culture in CD40 ligand and IL-4, transduced at high frequency with recombinant P501S in the vector pBIB, and selected with blastocidin-S. For *in vitro* priming, purified CD8+ T cells were cultured with autologous CD40
10 ligand + IL-4 derived, P501S-transduced B cells in a 96-well microculture format. These CTL microcultures were re-stimulated with P501S-transduced B cells and then assayed for specificity. Following this initial screen, microcultures with significant signal above background were cloned on autologous EBV-transformed B cells (BLCL), also transduced with P501S. Using IFN-gamma ELISPOT for detection, several of these CD8 T cell clones were found to be specific for P501S, as
15 demonstrated by reactivity to BLCL/P501S but not BLCL transduced with control antigen. It was further demonstrated that the anti-P501S CD8 T cell specificity is HLA-A2-restricted. First, antibody blocking experiments with anti-HLA-A,B,C monoclonal antibody (W6.32), anti-HLA-B,C monoclonal antibody (B1.23.2) and a control monoclonal antibody showed that only the anti-HLA-A,B,C antibody blocked recognition of P501S-expressing autologous BLCL. Secondly, the anti-
20 P501S CTL also recognized an HLA-A2 matched, heterologous BLCL transduced with P501S, but not the corresponding EGFP transduced control BLCL.

EXAMPLE 13

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

25 This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in
30 prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences

SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

5

Table I
Summary of Prostate Tumor Antigens

Known Genes	Previously Identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-Iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang (23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-idoitol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97%

of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

EXAMPLE 14

IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate-specific antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which

expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II
Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups:

10 Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones derived from the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones derived from the Plus, Minus and Other group libraries, but the number of ESTs derived from the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones derived from Plus, Minus and Other group

15 libraries, but the number derived from the Plus group is higher than the number derived from the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The EST clone inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high levels of tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor and normal prostate mRNA was at least three times the level in other normal tissue mRNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NO: 401-453, with certain novel sequences shown in SEQ ID NO: 407, 413, 416-419, 422, 426, 427 and 450.

Table IV
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57
439	22851	PAP

440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

EXAMPLE 15

FURTHER IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

5

This Example describes the isolation of additional prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NO: 454-467. Of these sequences, SEQ ID NO: 459-461 represent novel genes. The others (SEQ ID NO: 454-458 and 461-467) correspond to known sequences.

15

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE-SPECIFIC ANTIGEN P710P

20

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane

filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic Perkin Elmer/Applied Biosystems Division Sequencer. Four
5 sequences were obtained, and are presented in SEQ ID NO: 468-471. These sequences appear to represent different splice variants of the P710P gene.

EXAMPLE 17

PROTEIN EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10 This example describes the expression and purification of the prostate-specific antigen P501S in *E. coli*, baculovirus and mammalian cells.

a) Expression in *E. coli*

15 Expression of the full-length form of P501S was attempted by first cloning P501S without the leader sequence (amino acids 36-553 of SEQ ID NO: 113) downstream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) in pET17b. Specifically, P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW003 (SEQ ID NO: 486). AW025 is a sense cloning primer that contains a HindIII site. AW003 is an
20 antisense cloning primer that contains an EcoRI site. DNA amplification was performed using 5 µl 10X Pfu buffer, 1 µl 20 mM dNTPs, 1 µl each of the PCR primers at 10 µM concentration, 40 µl water, 1 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 95°C was performed for 30 sec, followed by 10 cycles of 95°C for 30 sec, 60°C for 1 min and by 72°C for 3 min. 20 cycles of 95°C for 30 sec, 65°C for 1 min and by 72°C for 3 min,
25 and lastly by 1 cycle of 72°C for 10 min. The PCR product was cloned to Ra12m/pET17b using HindIII and EcoRI. The sequence of the resulting fusion construct (referred to as Ra12-P501S-F) was confirmed by DNA sequencing.

The fusion construct was transformed into BL21(DE3)pLysE, pLysS and CodonPlus
E. coli (Stratagene) and grown overnight in LB broth with kanamycin. The resulting culture was
30 induced with IPTG. Protein was transferred to PVDF membrane and blocked with 5% non-fat milk (in PBS-Tween buffer), washed three times and incubated with mouse anti-His tag antibody (Clontech) for 1 hour. The membrane was washed 3 times and probed with HRP-Protein A

(Zymed) for 30 min. Finally, the membrane was washed 3 times and developed with ECL (Amersham). No expression was detected by Western blot. Similarly, no expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage (Invitrogen).

5 An N-terminal fragment of P501S (amino acids 36-325 of SEQ ID NO: 113) was cloned down-stream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 in pET17b as follows. P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW027 (SEQ ID NO: 487). AW027 is an antisense cloning primer that contains an EcoRI site and a stop codon. DNA amplification was performed essentially as described above. The resulting PCR
10 product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The fusion construct (referred to as Ra12-P501S-N) was confirmed by DNA sequencing.

The Ra12-P501S-N fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, essentially as described above. Using Western blot analysis, protein bands were observed at the expected molecular weight of 36 kDa. Some high molecular weight bands
15 were also observed, probably due to aggregation of the recombinant protein. No expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage.

A fusion construct comprising a C-terminal portion of P501S (amino acids 257-553 of SEQ ID NO: 113) located down-stream of the first 30 amino acids of the *M. tuberculosis* antigen
20 Ra12 (SEQ ID NO: 484) was prepared as follows. P501S DNA was used to perform PCR using the primers AW026 (SEQ ID NO: 488) and AW003 (SEQ ID NO: 486). AW026 is a sense cloning primer that contains a HindIII site. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The sequence for the fusion construct (referred to as Ra12-P501S-C) was confirmed.

25 The Ra12-P501S-C fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, as described above. A small amount of protein was detected by Western blot, with some molecular weight aggregates also being observed. Expression was also detected by Western blot when the Ra12-P501S-C fusion was used for expression in BL21CodonPlus induced by CE6 phage.

b) Expression of P501S in Baculovirus

The Bac-to-Bac baculovirus expression system (BRL Life Technologies, Inc.) was used to express P501S protein in insect cells. Full-length P501S (SEQ ID NO: 113) was amplified by PCR and cloned into the XbaI site of the donor plasmid pFastBacI. The recombinant bacmid and baculovirus were prepared according to the manufacturer's instructions. The recombinant baculovirus was amplified in Sf9 cells and the high titer viral stocks were utilized to infect High Five cells (Invitrogen) to make the recombinant protein. The identity of the full-length protein was confirmed by N-terminal sequencing of the recombinant protein and by Western blot analysis (Figure 7). Specifically, 0.6 million High Five cells in 6-well plates were infected with either the unrelated control virus BV/ECD_PD (lane 2), with recombinant baculovirus for P501S at different amounts or MOIs (lanes 4-8), or were uninfected (lane 3). Cell lysates were run on SDS-PAGE under reducing conditions and analyzed by Western blot with the anti-P501S monoclonal antibody P501S-10E3-G4D3 (prepared as described below). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

The localization of recombinant P501S in the insect cells was investigated as follows. The insect cells overexpressing P501S were fractionated into fractions of nucleus, mitochondria, membrane and cytosol. Equal amounts of protein from each fraction were analyzed by Western blot with a monoclonal antibody against P501S. Due to the scheme of fractionation, both nucleus and mitochondria fractions contain some plasma membrane components. However, the membrane fraction is basically free from mitochondria and nucleus. P501S was found to be present in all fractions that contain the membrane component, suggesting that P501S may be associated with plasma membrane of the insect cells expressing the recombinant protein.

c) Expression of P501S in mammalian cells

Full-length P501S (553AA) was cloned into various mammalian expression vectors, including pCEP4 (Invitrogen), pVR1012 (Vical, San Diego, CA) and a modified form of the retroviral vector pBMN, referred to as pBIB. Transfection of P501S/pCEP4 and P501S/pVR1012 into HEK293 fibroblasts was carried out using the Fugene transfection reagent (Boehringer Mannheim). Briefly, 2 ul of Fugene reagent was diluted into 100 ul of serum-free media and incubated at room temperature for 5-10 min. This mixture was added to 1 ug of P501S plasmid DNA, mixed briefly and incubated for 30 minutes at room temperature. The Fugene/DNA mixture

was added to cells and incubated for 24-48 hours. Expression of recombinant P501S in transfected HEK293 fibroblasts was detected by means of Western blot employing a monoclonal antibody to P501S.

Transfection of p501S/pCEP4 into CHO-K cells (American Type Culture Collection, Rockville, MD) was carried out using GenePorter transfection reagent (Gene Therapy Systems, San Diego, CA). Briefly, 15 μ l of GenePorter was diluted in 500 μ l of serum-free media and incubated at room temperature for 10 min. The GenePorter/media mixture was added to 2 μ g of plasmid DNA that was diluted in 500 μ l of serum-free media, mixed briefly and incubated for 30 min at room temperature. CHO-K cells were rinsed in PBS to remove serum proteins, and the GenePorter/DNA mix was added and incubated for 5 hours. The transfected cells were then fed an equal volume of 2x media and incubated for 24-48 hours.

FACS analysis of P501S transiently infected CHO-K cells, demonstrated surface expression of P501S. Expression was detected using rabbit polyclonal antisera raised against a P501S peptide, as described below. Flow cytometric analysis was performed using a FaCScan (Becton Dickinson), and the data were analyzed using the Cell Quest program.

EXAMPLE 18

PREPARATION AND CHARACTERIZATION OF ANTIBODIES AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

20 a) Preparation and Characterization of Antibodies against P501S

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO: 113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody component were sacrificed and spleen cells were used to

generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant ($\mu\text{g/ml}$)
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis. Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1 $\mu\text{g/ml}$, followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate

specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with P501S or HLA-B8 as a control antigen and either fixed and permeabilized as described above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity than DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically recognizes P501S in these tumor cell lines and that the epitope recognized in prostate tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145 cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr.

HRP-labeled anti-mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L) Affinipure F(ab') fragment (Jackson Immunoresearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors, 5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

b) Preparation and Characterization of Antibodies against P503S

A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits

and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

5

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows.

The recombinant fragment of P503S that was employed as the immunogen was used as a positive control. Ninety-six well microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in PBST were added to the wells and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further

15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

Subsequent to epitope mapping, the antibodies were tested by FACS analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to cell surface epitopes. Cells stably transfected with a control plasmid were employed as a negative control. Cells were stained live with no fixative. 0.5 ug of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat anti-rabbit or mouse secondary antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a panel of normal tissues (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum and kidney, and no expression being observed in adrenal, breast, duodenum, gall bladder, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full length P503S. Protein was transferred to nitrocellulose and then Western blotted with each of the anti-P503S monoclonal antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the

appropriate molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

5 **c) Preparation and Characterization of Antibodies against P703P**

Rabbits were immunized with either a truncated (P703Ptr1; SEQ ID NO: 172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptr1 attached to a solid support. Rabbit monoclonal
10 antibodies were isolated using SLAM technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal and monoclonal antibodies that were generated against P703P.

Table VII

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptr1	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptr1	Rabbit monoclonal
8H2	P703Ptr1	Rabbit monoclonal
7H8	P703Ptr1	Rabbit monoclonal

15

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and are provided in SEQ ID NO: 506-508, respectively.

Epitope mapping studies were performed as described above. Monoclonal
20 antibodies 2D4 and 7H8 were found to specifically bind to the peptides of SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively. The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

25 The specificity of the anti-P703P antibodies was determined by Western blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed recombinant antigen; (2) lysates of HEK293 cells and Ltk^{-/-} cells either untransfected or transfected with a plasmid

expressing full length P703P; and (3) supernatant isolated from these cell cultures. Protein was transferred to nitrocellulose and then Western blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight since it is epitope tagged. In lysates and supernatants from cells transfected with full length P703P, a 30 kDa band corresponding to P703P was observed. To assure specificity, lysates from HEK293 cells stably transfected with a control plasmid were also tested and were negative for P703P expression. Other anti-P703P antibodies showed similar results.

Immunohistochemical studies were performed as described above, using anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in normal prostate and prostate tumor tissue but was not detectable in all other tissues tested (breast tumor, lung tumor and normal kidney).

EXAMPLE 19

CHARACTERIZATION OF CELL SURFACE EXPRESSION AND CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

This example describes studies demonstrating that the prostate-specific antigen P501S is expressed on the surface of cells, together with studies to determine the probable chromosomal location of P501S.

The protein P501S (SEQ ID NO: 113) is predicted to have 11 transmembrane domains. Based on the discovery that the epitope recognized by the anti-P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is intracellular, it was predicted that following transmembrane determinants would allow the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation of the P501S protein showing the predicted location of the transmembrane domains and the intracellular epitope described in Example 17. Underlined sequence represents the predicted transmembrane domains, bold sequence represents the predicted extracellular domains, and italicized sequence represents the predicted intracellular domains. Sequence that is both bold and underlined represents sequence employed to generate polyclonal rabbit serum. The location of the transmembrane domains was predicted using HHMTOP as

described by Tusnady and Simon (Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction, *J. Mol. Biol.* 283:489-506, 1998).

Based on Fig. 9, the P501S domain flanked by the transmembrane domains corresponding to amino acids 274-295 and 323-342 is predicted to be extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519, which is identical to the peptide of SEQ ID NO: 518 with the exception of the substitution of the histidine with an asparagine, was synthesized as described above. A Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether. The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described above.

Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 µg/ml, washed, incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (i.e. intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of homogenization buffer (250 mM

sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1 complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C. Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30 min at 4 °C to recover peripheral membrane. Samples were then separated by SDS-PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3 (described above in Example 17) using conditions described above. Recombinant purified P501S, as well as HEK293 cells transfected with and over-expressing P501S were included as positive controls for P501S detection. LCL cell lysate was included as a negative control. P501S could be detected in Lncap total cell lysate, the 8000g (internal membrane) fraction and also in the 100,000g (plasma membrane) fraction. These results indicate that P501S is expressed at, and localizes to, the peripheral membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed. For these analyses, flat-bottomed 96 well microtiter plates were coated with either the peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment (corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the immunizing peptide sequence, at 1 µg/ml for 2 hours at 37 °C. Wells were aspirated, blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng - 125 ng) in PBST and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates were then washed and incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above.

To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed through the Whitehead Institute/MIT Center for Genome Research web server (<http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al. Science* 274:1371-1374, 1996 and Berthon *et al. Am. J. Hum. Genet.* 62:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

25

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

30

CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate-specific protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID No: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534 and 537-550.

4. An isolated polynucleotide encoding at least 15 contiguous amino acid residues of a prostate-specific protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the protein
5 comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413,
10 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate-specific protein, or a
15 variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396,
20 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one
25 of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530,
30 531, 533, 535 and 536.

7. An isolated polynucleotide comprising a sequence that hybridizes under moderately stringent conditions to a sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-8.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate-specific protein, the protein comprising an amino acid sequence encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471, 472-476, 524, 526, 530, 531, 533, 535 and 536 or a complement of any of the foregoing polynucleotide sequences.

12. A monoclonal antibody that specifically binds to an amino acid sequence selected from the group consisting of SEQ ID NO: 496, 504, 505, 509-517, 519, 520, 522 and 539-551.

5 13. A monoclonal antibody comprising a complementarity determining region selected from the group consisting of SEQ ID NO: 502, 503 and 506-508.

10 14. A fusion protein comprising at least one polypeptide according to claim 1.

15 15. A fusion protein according to claim 14, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

16 16. A fusion protein according to claim 14, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

20 17. A fusion protein according to claim 14, wherein the fusion protein comprises an affinity tag.

18. An isolated polynucleotide encoding a fusion protein according to claim 14.

25 19. A pharmaceutical composition comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to any one of claims 11-13;
- 30 (d) a fusion protein according to claim 14; and

(e) a polynucleotide according to claim 18.

20. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- 5 (a) a polypeptide according to claim 1;
(b) a polynucleotide according to claim 4;
(c) an antibody according to any one of claims 11-13;
(d) a fusion protein according to claim 14; and
(e) a polynucleotide according to claim 18.

10

21. A vaccine according to claim 20, wherein the immunostimulant is an adjuvant.

22. A vaccine according to claim 20, wherein the immunostimulant
15 induces a predominantly Type I response.

23. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 19.

20

24. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 20.

25. A pharmaceutical composition comprising an antigen-presenting cell
25 that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

26. A pharmaceutical composition according to claim 25, wherein the antigen presenting cell is a dendritic cell or a macrophage.

27. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with an immunostimulant.

5 28. A vaccine according to claim 27, wherein the immunostimulant is an adjuvant.

29. A vaccine according to claim 27, wherein the immunostimulant induces a predominantly Type I response.

10 30. A vaccine according to claim 27, wherein the antigen-presenting cell is a dendritic cell.

31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide encoded by a polynucleotide recited in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, and thereby inhibiting the development of a cancer in the patient.

20 32. A method according to claim 31, wherein the antigen-presenting cell is a dendritic cell.

33. A method according to any one of claims 23, 24 and 31, wherein the cancer is prostate cancer.

25 34. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536; and

(ii) complements of the foregoing polynucleotides;

5 wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate-specific protein from the sample.

35. A method according to claim 34, wherein the biological sample is
10 blood or a fraction thereof.

36. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

15

37. A method for stimulating and/or expanding T cells specific for a prostate-specific protein, comprising contacting T cells with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;

20 (ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;

(iii) a polynucleotide encoding a polypeptide of (i) or (ii); and

(iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii),

25 under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

38. An isolated T cell population, comprising T cells prepared according to the method of claim 37.

30

39. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 38.

5 40. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;

10 (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;

(iii) a polynucleotide encoding a polypeptide of (i) or (ii); or

15 (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

20 41. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

25 (i) a polypeptide according to claim 1;

(ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536;

30 (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or

(iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

(b) cloning at least one proliferated cell to provide cloned T cells; and

5 (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

42. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

10 (a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NO: 1-111,
15 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536; and

(ii) complements of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

20 (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

43. A method according to claim 42, wherein the binding agent is an antibody.

25

44. A method according to claim 43, wherein the antibody is a monoclonal antibody.

45. A method according to claim 42, wherein the cancer is prostate
30 cancer.

46. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- 5 (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;
- 10 (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polypeptide detected in step (c) to the
15 amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

47. A method according to claim 46, wherein the binding agent is an antibody.

20 48. A method according to claim 47, wherein the antibody is a monoclonal antibody.

49. A method according to claim 46, wherein the cancer is a prostate
25 cancer.

50. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient with an
30 oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein,

wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;

5 (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

10

51. A method according to claim 50, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

15

52. A method according to claim 50, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

20

53. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate-specific protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence of any one of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 25 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from 30 the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

5 54. A method according to claim 53, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

10 55. A method according to claim 53, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

 56. A diagnostic kit, comprising:
 (a) one or more antibodies according to claim 11; and
15 (b) a detection reagent comprising a reporter group.

 57. A kit according to claim 56, wherein the antibodies are immobilized on a solid support.

20 58. A kit according to claim 56, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

 59. A kit according to claim 56, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups,
25 enzymes, biotin and dye particles.

 60. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate-specific protein, wherein the protein comprises an amino acid sequence that is
30 encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45,

47-52, 54-65; 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-476, 524, 526, 530, 531, 533, 535 and 536, or a complement of any of the foregoing polynucleotides.

61. A oligonucleotide according to claim 60, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-476, 524, 526, 530, 531, 533, 535 and 536.

15

62. A diagnostic kit, comprising:

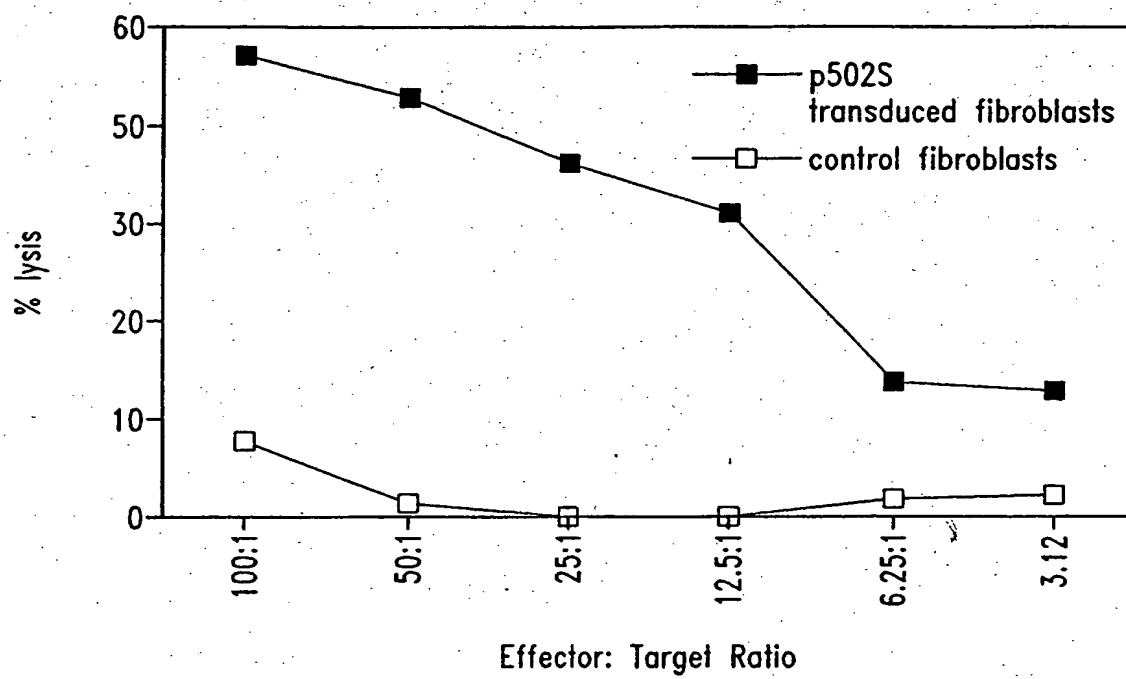
- (a) an oligonucleotide according to claim 61; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

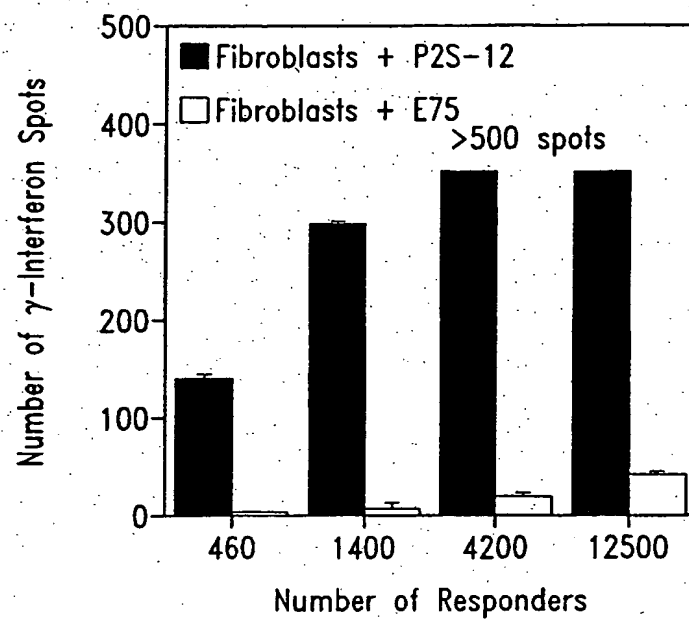
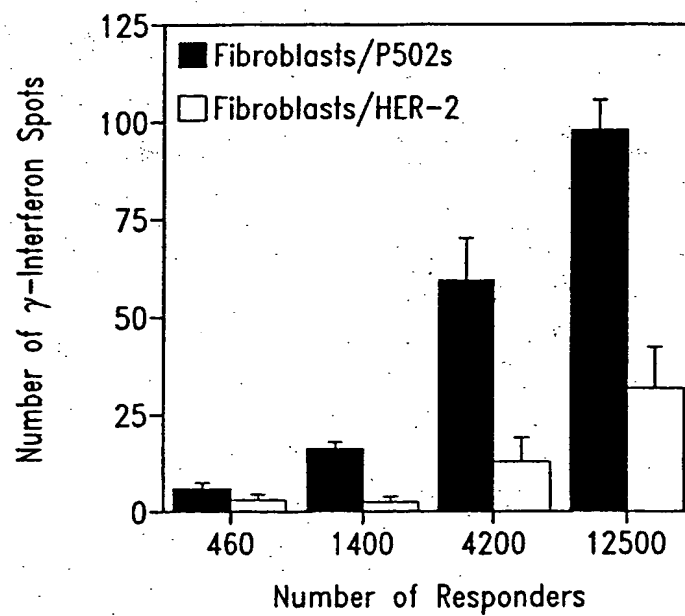
20

63. A host cell according to claim 10, wherein the cell is selected from the group consisting of: *E. coli*, baculovirus and mammalian cells.

64. A recombinant protein produced by a host cell according to claim 10.

25

*Fig. 1*

*Fig. 2A**Fig. 2B*

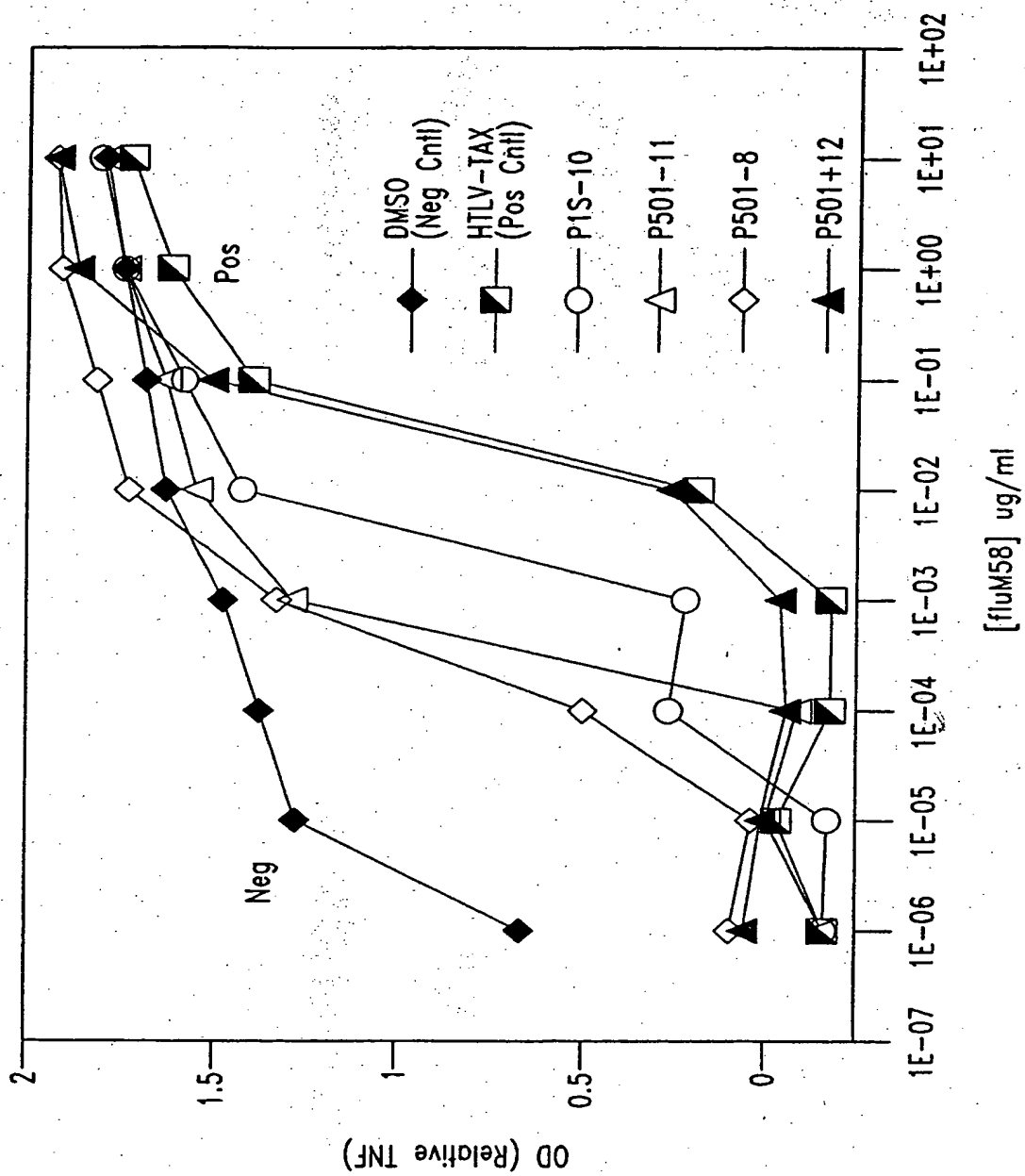
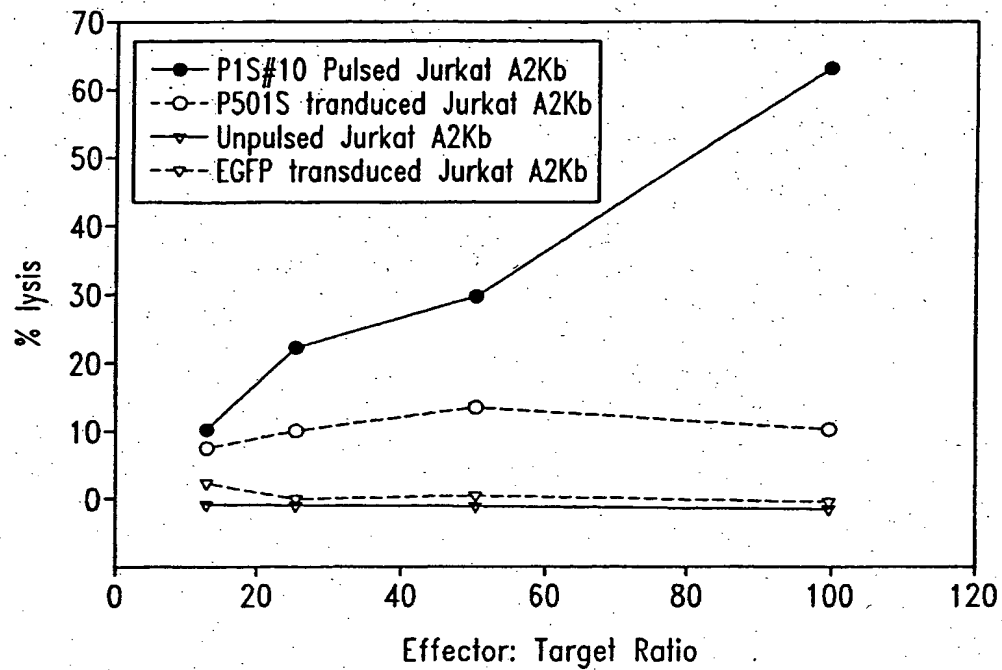
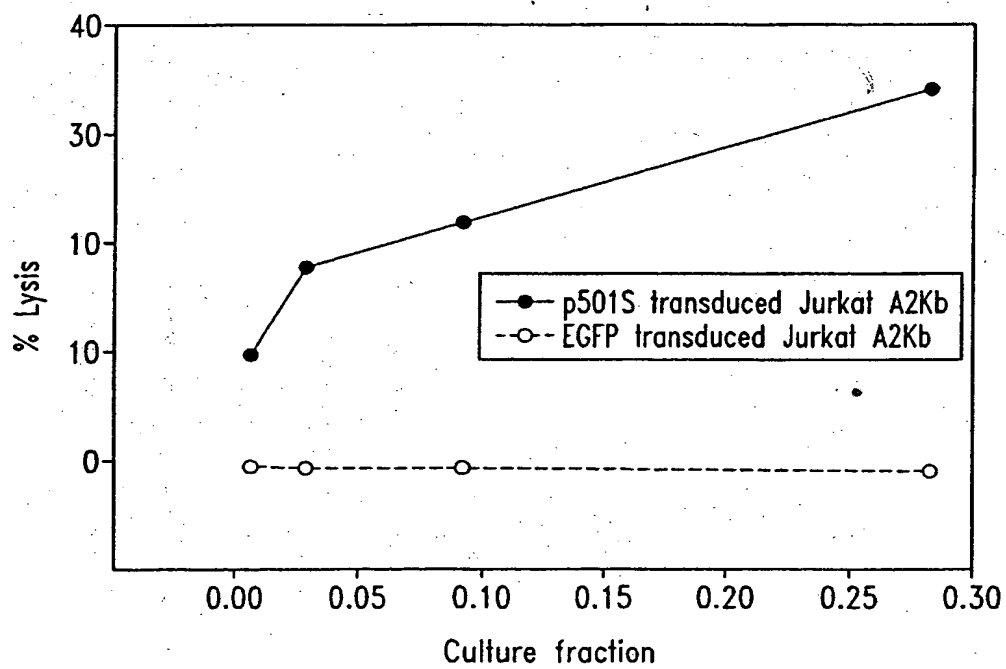
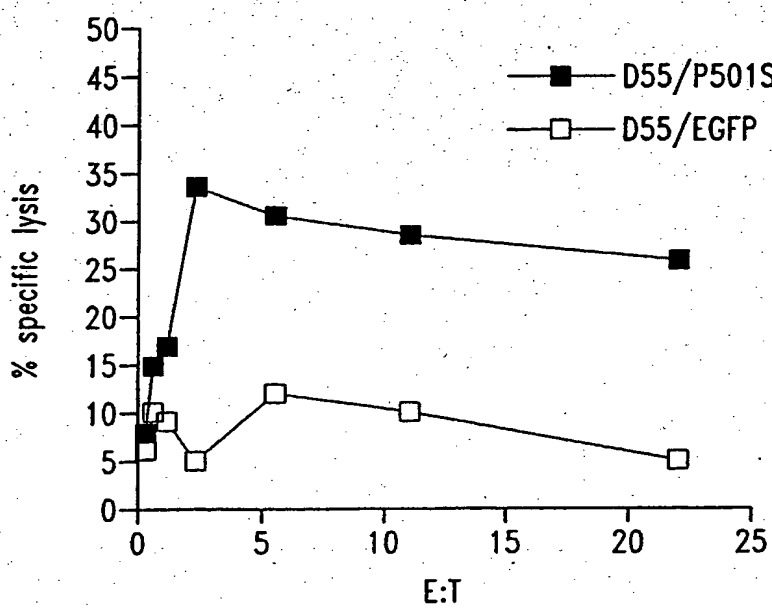
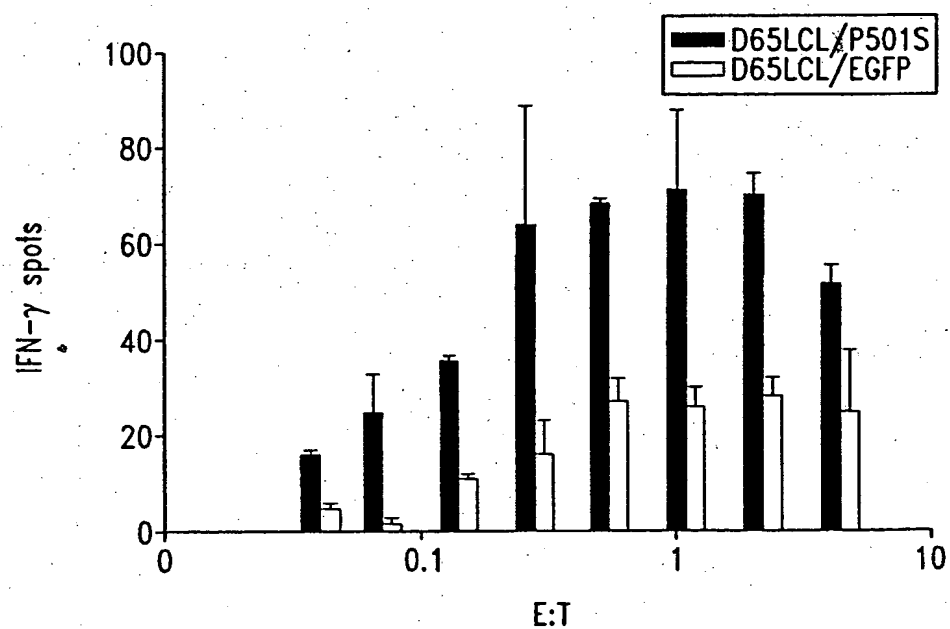
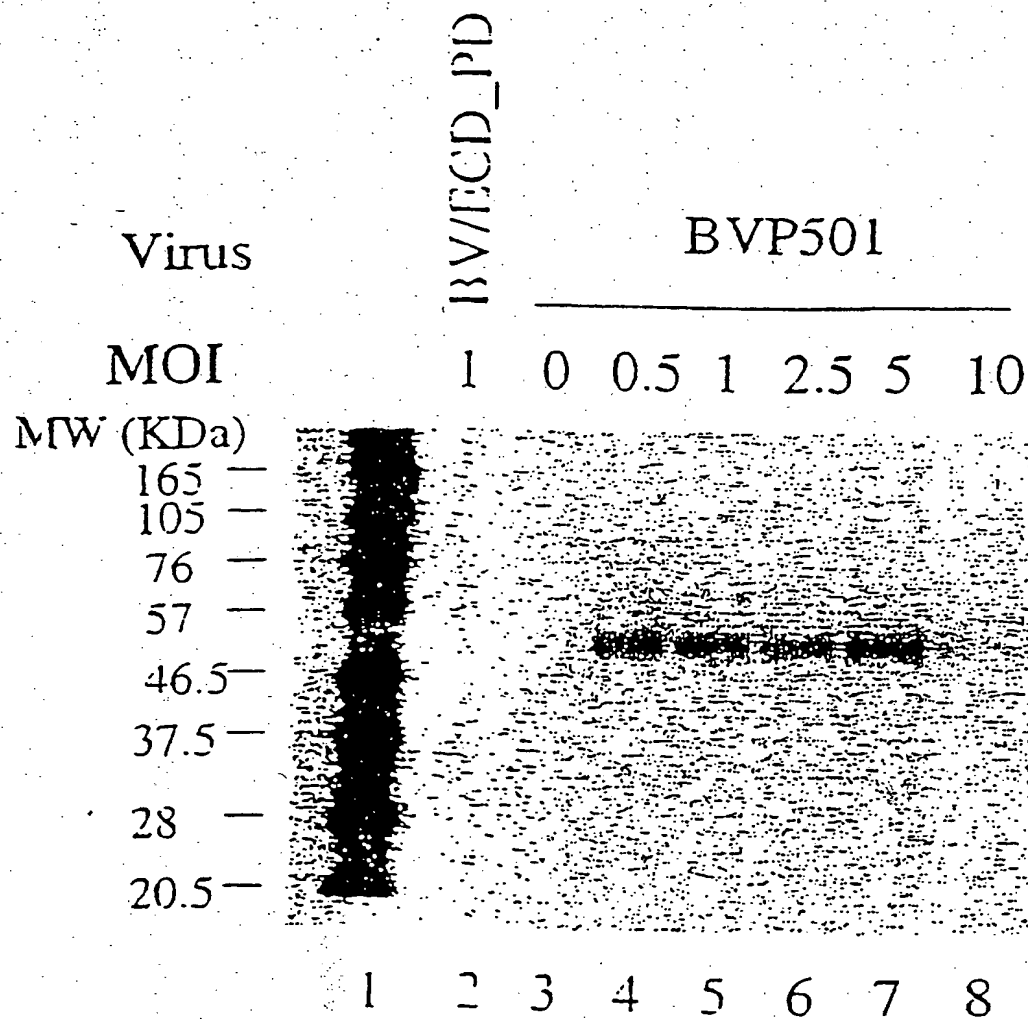


Fig. 3

*Fig. 4**Fig. 5*

*Fig. 6A**Fig. 6B*

Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 - 8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

Schematic of P501S with predicted
transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT **YVPPLLLLEVGVEEKFM**
TMVLGIGPVLGLVCYPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL **AGLLCPDPRPLE** LALLILGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRCQ AYSVYAFMISLGGCLGYLLPAI **DWDTSALAPYLGTQEE**

CLFGLLTILFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPTLRR LFVAELCSWMALMTFTLFYTDF VGEGLYQGVPRAEPTARRHYDEGVR

MGSLGLFLQCAISLVFSLVM *DRLVQRFQTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA **SAA**

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSED* **SLMTSFLPGPKPGAPFPNGHVGAGGSGL**

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**

VTAYMVSAAGLGLVAIYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence**:
Predicted extracellular domain; *Italic sequence*: Predicted intracellular
domain. Sequence in bold/underlined: used generate polyclonal rabbit
serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon
(1998) Principles Governing Amino Acid Composition of Integral Membrane
Proteins: Applications to topology Prediction. J. Mol Biol. 283, 489-506.

Fig. 9

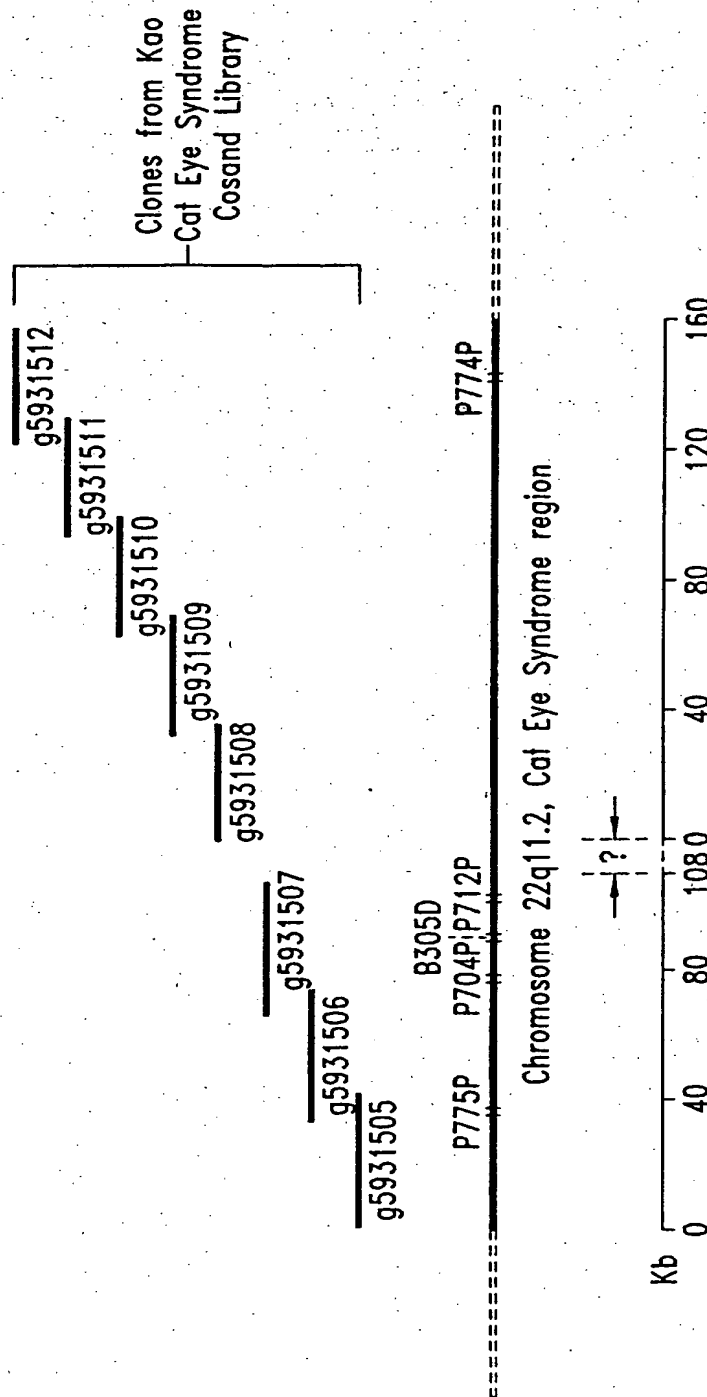


Fig. 10

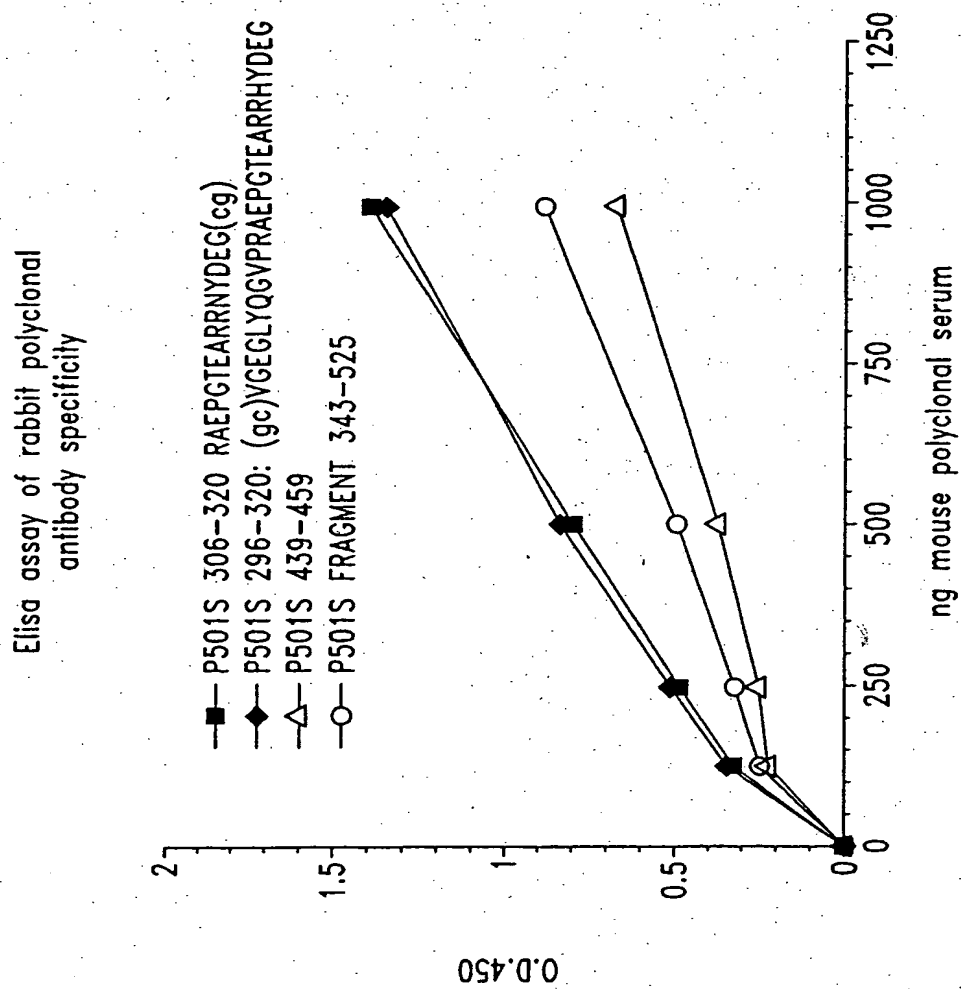


Fig. 11

SEQUENCE LISTING

<110> Corixa Corporation
 Xu, Jiangchun
 Dillon, Davin C.
 Mitcham, Jennifer L.
 Harlocker, Susan Louise
 Jiang Yuqui
 Reed, Steven G.
 Kalos, Michael
 Fanger, Gary
 Retter, Mark
 Solk, John
 Day, Craig
 Skeiky, Yasir A.W.
 Wang, Aijun

<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND
 DIAGNOSIS OF PROSTATE CANCER

<130> 210121.42720PC

<140> PCT

<141> 2000-11-09

<160> 551

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 814

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(814)

<223> n = A,T,C or G

<400> 1

tttttttttt	tttttcacag	tataacagct	ctttatttct	gtgagttcta	ctaggaaatc	60
atcaaactctg	agggttgtct	ggaggacttc	aatacacctc	cccccatagt	gaatcagctt	120
ccaggggggtc	cagtcctctc	ccttacttca	tccccatccc	atgccaaagg	aagacctctc	180
ctccttggct	cacagccttc	tctaggcttc	ccagtgcctc	caggacagag	tgggttatgt	240
tttcagctcc	atccttgctg	tgagtgtctg	gtgcgttggtg	cctccagctt	ctgctcagtg	300
cttcattggac	agtgtccagc	acatgtcact	ctccactctc	tcagtgtgga	tccactagtt	360
ctagagcggc	cgccaccgcg	gtggagctcc	agcttttgtt	cccttttagtg	agggttaatt	420
gcgcgcttgg	cgtaatcatg	gtcataactg	tttcctgtgt	gaaattgtta	tccgctcaca	480
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaatgagtg	540
anctaactca	cattaattgc	gttgcgctca	ctgnccgctt	tccagtcnng	aaaactgtcg	600
tgccagctgc	attaatgaat	cggccaacgc	ncggggaaaa	gcggtttgcg	ttttgggggc	660
tcttcgcgtt	ctcgtctcact	nantcctgcg	ctcggtcntt	cggtctgcggg	gaacgggtatc	720
actcctcaaa	gngngtatta	cggttatccn	naaatcnngg	gatacccnng	aaaaaanttt	780
aacaaaaggg	cancaaaggg	cngaaacgta	aaaa			814

<210> 2

<211> 816

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(816)

<223> n = A,T,C or G

<400> 2

acagaaatgt	tggatggtgg	agcacctttc	tatacgactt	acaggacagc	agatggggaa	60
ttcatggctg	ttggagcaat	agaaccccag	ttctacgagc	tgctgatcaa	aggacttgga	120
ctaaagtctg	atgaacttcc	caatcagatg	agcatggatg	attggccaga	aatgaagaag	180
aagtttgcag	atgtatttgc	aaagaagacg	aaggcagagt	ggtgtcaaat	ctttgacggc	240
acagatgcct	gtgtgactcc	ggttctgact	tttgaggagg	ttgttcatca	tgatcacaa	300
aaggaacggg	gctcgtttat	caccagttag	gagcaggacg	tgagcccccg	ccctgcacct	360
ctgctgttaa	acaccccagc	catcccttct	ttcaaaaggg	atccactagt	tctagaagcg	420
gccgccaccg	cgggtggagct	ccagcttttg	ttccctttag	tgagggttaa	ttgcgcgctt	480
ggcgtaatca	tggtcatagc	tgtttctctg	gtgaaattgt	tatccgctca	caattcccc	540
aacatacgag	cgggaacata	aagtgttaag	cctgggggtgc	ctaattgantg	agctaactcn	600
cattaattgc	gttgcgctca	ctgcccgcct	tccagtcggg	aaaactgtcg	tgccactgcn	660
ttantgaatc	ngccaccccc	cgggaaaagg	cggttgcntt	ttgggcctct	tccgctttcc	720
tcgctcattg	atcctngcnc	cgggtcttcg	gctgcggnga	acggttcact	cctcaaaggg	780
ggtntnccgg	ttatccccaa	acnggggata	cccnga			816

<210> 3

<211> 773

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(773)

<223> n = A,T,C or G

<400> 3

cttttgaaag	aagggatggc	tgggggtggtt	aacagcagag	gtgcagggcg	ggggctcacg	60
tctgtctcct	cactgggtgat	aaacgagccc	cgttccttgt	tgtgatcatg	atgaacaacc	120
tcttcaaaag	tcagaaccgg	agtcacacag	gcattctgtg	cgtcaaagat	ttgacaccac	180
tctgccttcg	tcttctttgc	aaatacatct	gcaaacttct	tcttcatttc	tgcccaatca	240
tccatgetca	tctgattggg	aagttcatca	gactttagtc	canntccttt	gacagcagc	300
tcgtagaact	ggggttctat	tgctccaaca	gccatgaatt	ccccatctgc	tgctctgtaa	360
gtcgtataga	aaggtgctcc	accatccaac	atgttctgtc	ctcgaggggg	ggcccgggtac	420
ccaattcgcc	ctatantgag	tcgtattacg	cgcgctcact	ggccgctcgtt	ttacaacgct	480
gtgactggga	aaaccctggg	cgttaccaac	ttaatcgctt	tgacgacat	ccccctttcg	540
ccagctgggc	gtaatanega	aaaggcccg	accgatcgcc	cttccaacag	ttgcgcacct	600
gaatgggnaa	atgggacccc	cctgttaccg	cgcattnaac	ccccgcnggg	tttngttggt	660
acccccacnt	nnaccgctta	cactttgcc	gcgccttanc	gcccgcctcc	tttncctttt	720
cttcccttcc	tttncnccn	ctttcccccg	gggtttcccc	cntcaaaccc	cna	773

<210> 4

<211> 828

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(828)

<223> n = A,T,C or G

<400> 4

cctcctgagt	cctactgacc	tgtgctttct	ggtgtggagt	ccagggctgc	taggaaaagg	60
aatgggcaga	cacaggtgta	tgccaatgtt	tctgaaatgg	gtataatttc	gtcctctcct	120
tcggaacact	ggctgtctct	gaagacttct	cgctcagttt	cagtgaggac	acacacaaag	180
acgtgggtga	ccatgttgtt	tgtgggggtgc	agagatggga	gggggtggggc	ccaccctgga	240
agagtggaca	gtgacacaag	gtggacactc	tctacagatc	actgaggata	agctggagcc	300
acaatgcatg	aggcacacac	acagcaagga	tgacnctgta	aacatagccc	acgctgtcct	360
gngggcactg	ggaagcctan	atnaggccgt	gagcanaaag	aaggggagga	tccactagtt	420
ctanagcggc	cgccaccgcg	gtgganctcc	ancttttgtt	cccttttagtg	agggttaatt	480
gcgcgcttgg	cmtaatcatg	gtcatanctn	tttctgtgtg	gaaattgtta	tccgctcaca	540
attccacaca	acatacganc	cggaacata	aantgtaaac	ctgggggtgcc	taatgantga	600
ctaactcaca	ttaattgcgt	tgcgctcact	gcccgccttc	caatcnggaa	acctgtcttg	660
ccncttgcct	tnatgaatcn	gccaaacccc	ggggaaaagc	gtttgcgttt	tgggcgctct	720
tccgcttcct	cnctcantta	ntccctncnc	tcggtcattc	cggctgcngc	aaaccggttc	780
accnctcca	aaggggggtat	tccggtttcc	ccnaatccgg	gganancc		828

<210> 5

<211> 834

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(834)

<223> n = A,T,C or G

<400> 5

tttttttttt	tttttactga	tagatggaat	ttattaagct	tttcacatgt	gatagcacat	60
agtttttaatt	gcatccaaag	tactaacaâa	aactctagca	atcaagaatg	gcagcatgtt	120
atttttataac	aatcaacacc	tgtggccttt	aaaattttggt	tttcataaga	taattttatac	180
tgaagtaaat	ctagccatgc	ttttaaaaaa	tgcttttaggt	cactccaagc	ttggcagtta	240
acattttggca	taaaacaata	taaaacaatc	acaattttaat	aaataacaaa	tacaacattg	300
tagggcataa	tcatatacag	tataaggaaa	aggtggtagt	gttgagtaag	cagttattag	360
aatagaatac	cttggcctct	atgcaaatat	gtctagacac	tttgattcac	tcagccctga	420
cattcagttt	tcaaagtagg	agacagggtc	tacagtatca	ttttacagtt	tccaacacat	480
tgaaaacaag	tagaaaatga	tgagttgatt	tttattaatg	cattacatcc	tcaagagtta	540
tcaccaaccc	ctcagttata	aaaaattttc	aagttatatt	agtcataata	cttggtgtgc	600
ttatttttaa	ttagtgtctaa	atggattaag	tgaagacaac	aatgggtccc	taatgtgatt	660
gatattggtc	atttttacca	gcttctaaat	ctnaactttc	aggcttttga	actggaacat	720
tgnatnacag	tgttccanag	ttncaaccta	ctggaacatt	acagtgtgct	tgattcaaaa	780
tgttattttg	ttaaaaatta	aatttttaacc	tggtggaaaa	ataatttgaa	atna	834

<210> 6

<211> 818

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(818)

<223> n = A,T,C or G

<400> 6

tttttttttt	tttttttttt	aagaccctca	tcaatagatg	gagacataca	gaaatagtca	60
aaccacatct	acaaaatgcc	agtatcaggc	ggcggcttcg	aagccaaagt	gatgttttga	120
tgtaaagtga	aatattagtt	ggcggatgaa	gcagatagtg	aggaaaagttg	agccaataat	180
gacgtgaagt	ccgtggaagc	ctgtggctac	aaaaaatgtt	gagccgtaga	tgccgctcga	240
aatggtgaag	ggagactcga	agtactctga	ggcttgttagg	agggtaaaaat	agagacccag	300

taaaattgta	ataagcagtg	cttgaattat	ttggtttcgg	ttgttttcta	ttagactatg	360
gtgagctcag	gtgattgata	ctcctgatgc	gagtaatacg	gatgtgttta	ggagtgggac	420
ttctagggga	tttagcgggg	tgatgcctgt	tgggggccag	tgccctccta	gttggggggg	480
aggggctagg	ctggagtggg	aaaaggctca	gaaaaatcct	gcgaagaaaa	aaacttctga	540
ggtaataaat	aggattatcc	cgtatcgaag	gccttttttg	acaggtgggt	tgtgggtggc	600
ttggtatgtg	ctttctcgtg	ttacatcgcg	ccatcattgg	tatatgtgta	gtgtgttggg	660
ttantangg	ctantatgaa	gaacttttgg	antggaatta	aatcaatngc	ttggccggaa	720
gtcattanga	nggctnaaaa	ggcctgttta	ngggtctggg	ctnggtttta	cccnacccat	780
ggaatncnc	ccccggacna	ntgnatccct	attcttaa			818

<210> 7

<211> 817

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (817)

<223> n = A,T,C or G

<400> 7

tttttttttt	tttttttttt	tggctctaga	gggggtagag	gggggtgctat	agggtaaata	60
cgggccctat	ttcaaagatt	tttaggggaa	ttaattctag	gacgatgggt	atgaaactgt	120
ggtttgctcc	acagatttca	gagcattgac	cgtagtatac	ccccggtcgt	gtagcgggtga	180
aagtggtttg	gttttagacgt	ccgggaattg	catctgtttt	taagcctaata	gtggggacag	240
ctcatgagtg	caagacgtct	tgtgatgtaa	ttattatacn	aatgggggct	tcaatcgga	300
gtactactcg	attgtcaacg	tcaaggagtc	gcaggtcgcc	tggttctagg	aataatgggg	360
gaagtatgta	ggaattgaag	attaatccgc	cgtagtcggt	gttctcctag	gttcaatacc	420
attggtggcc	aattgatttg	atggtaaggg	gagggatcgt	tgaactcgtc	tgttatgtaa	480
aggatncctt	ngggatggga	aggcnatnaa	ggactangga	tnaatggcgg	gcangatatt	540
tcaaacngtc	tctanttcct	gaaacgtctg	aaatgttaat	aanaattaan	tttngttatt	600
gaatnttnng	gaaaagggct	tacaggacta	gaaaccaa	angaaaanta	atnntaangg	660
cnttatcntn	aaaggtnata	accnctccta	tnatcccacc	caatngnatt	ccccacnenn	720
acnattggat	nccccanttc	canaaanggc	cnccccccg	tgnannccnc	cttttgttcc	780
cttnantgan	ggttattcnc	ccctngcntt	atcance			817

<210> 8

<211> 799

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (799)

<223> n = A,T,C or G

<400> 8

catttcggg	tttactttct	aaggaaagcc	gagcggaagc	tgctaacgtg	ggaatcggtg	60
cataaggaga	actttctgct	ggcacgcgct	agggacaagc	gggagagcga	ctccgagcgt	120
ctgaagcgca	cgtcccagaa	ggtggacttg	gcactgaaac	agctgggaca	catccgcgag	180
tacgaacagc	gcctgaaagt	gctggagcgg	gaggtccagc	agtgtagccg	cgtcctgggg	240
tgggtggccg	angcctganc	cgtctgcct	tgtgcccc	angtgggccc	ccacccctg	300
acctgcctgg	gtccaaacac	tgagccctgc	tggcggactt	caagganaac	ccccacangg	360
ggattttgct	cctanantaa	ggetcatctg	ggcctcggcc	ccccacctg	gttggccttg	420
tctttgangt	gagcccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
ctccttcaa	ccacannatg	ccggctcct	cccggaacc	antcccancc	tgngaaggat	540
caagnctcgn	atccactnnt	nectanaaccg	gccnccnccg	cngtgggaacc	gnccttntgt	600
tccttttct	tnagggttaa	tnnccgcttg	gccttnccan	ngtccctncc	nttttccnnt	660

gttnaaattg	ttangcnccc	nccnntcccn	cnnennnnan	cccgaccenn	annttnnann	720
ncctgggggt	nccnnngat	tgaccenncc	ncctntant	tgcnttnggg	nncntgccc	780
ctttccctct	nggganncg					799

<210> 9

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 9

acgccttgat	cctcccagge	tgggactggt	tctgggagga	gccggggcatg	ctgtgggttg	60
taangatgac	actcccaaag	gtggtcctga	cagtggccca	gatggacatg	gggctcacct	120
caaggacaag	gccaccaggt	gcggggggccg	aagcccacat	gacccctact	ctatgagcaa	180
aatcccctgt	gggggcttct	ccttgaagtc	cgccancagg	gctcagtctt	tggacccang	240
caggtcatgg	ggttgtnngc	caactggggg	ccncaacgca	aaanggcnc	gggcctcngn	300
cacccatccc	angacgcggc	tacactnctg	gacctccnc	tccaccactt	tcatgcgctg	360
ttcntaccgg	cgnatntgtc	ccanctgttt	cngtgcenac	tccancttct	nggacgtgcg	420
ctacatacgc	cggantcnc	netcccgttt	tgccctatc	cacgtncan	caacaaattt	480
cncntantg	cacnattcc	cacntttnc	agntttcnc	nncgncttc	ctntaaaag	540
ggttganccc	cggaaaatnc	cccaaagggg	ggggggcngg	tacccaactn	ccccctnata	600
gctgaantcc	ccatnaccnn	gnctcnatgg	ancntccnt	tttaannaen	ttctnaactt	660
gggaanance	ctcgnccntn	ccccenttaa	tccnccctg	cnangnnent	ccccnntcc	720
nccnnntng	gcntntnann	cnaaaaaggc	ccnnnancaa	tctcctnnen	cctcanttgc	780
ccanccctcg	aaatcgccn	c				801

<210> 10

<211> 789

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(789)

<223> n = A,T,C or G

<400> 10

cagtctatnt	ggccagtgtg	gcagctttcc	ctgtggctgc	cggtgccaca	tgccgtgtccc	60
acagtgtggc	cgtggtgaca	gcttcagccg	ccctcaccgg	gttcaccttc	tcagccctgc	120
agatccctgc	ctacacactg	gcctccctct	accaccggga	gaagcaggtg	ttcctgccc	180
aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	cctgatgacc	agcttccctgc	240
caggccctaa	gcctggagct	cccttcctta	atggacacgt	gggtgctgga	ggcagtggcc	300
tgctccccacc	tccaccgcg	ctctgcgggg	cctctgcctg	tgatgtctcc	gtacgtgtgg	360
tggtgggtga	gcccaccgan	gccagggtgg	ttccgggccc	gggcatctgc	ctggacctgc	420
ccatccctgga	tagtgcttcc	tgctgtccca	ngtggcccca	tcctgttta	tgggtccat	480
tgtccagctc	agccagctctg	tcactgccta	tatggtgtct	gccgcaggcc	tgggtctggt	540
cccatttact	ttgctacaca	ggtantattt	gacaagaacg	anttgcccaa	atactcagcg	600
ttaaaaaatt	ccagcaacat	tgggggtgga	aggcctgcct	cactgggtcc	aactccccgc	660
tcctgttaac	cccatggggc	tgccggcttg	gccgccaat	tctgttgctg	ccaaantnat	720
gtggctctct	gctgccacct	gttgcctggt	gaagtgcnta	cngcncanct	nggggggtng	780
ggngttccc						789

<210> 11

<211> 772

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(772)

<223> n = A,T,C or G

<400> 11

cccaccctac	ccaaatatta	gacaccaaca	cagaaaagct	agcaatggat	tcccttctac	60
tttggttaaat	aaataagtta	aatattttaa	tgcctgtgtc	tctgtgatgg	caacagaagg	120
accaacaggc	cacatcctga	taaaaggtaa	gaggggggtg	gatcagcaaa	aagacagtgc	180
tgtgggctga	ggggacctgg	ttcttgtgtg	ttgccccctca	ggactcttcc	cctacaaata	240
actttcatat	gttcaaatcc	catggaggag	tgtttcatcc	tagaaactcc	catgcaagag	300
ctacattaaa	cgaagctgca	ggtaagggg	cttanagatg	ggaaaccagg	tgactgagtt	360
tattcagctc	ccaaaaaccc	ttctctaggt	gtgtctcaac	taggaggcta	gctgttaacc	420
ctgagcctgg	gtaatccacc	tgcagagtcc	ccgcattcca	gtgcatggaa	cccttctggc	480
ctccctgtat	aagtccagac	tgaaccccc	ttggaaggnc	tccagtcagg	cagccctana	540
aactggggaa	aaaagaaaag	gacgccccan	ccccagctg	tgcantacg	cacctcaaca	600
gcacaggggtg	gcagcaaaaa	aaccacttta	ctttggcaca	aacaaaaact	ngggggggca	660
accccggcac	cccnangggg	gttaacagga	ancngggnaa	cntggaaccc	aattnaggca	720
ggcccncac	ccnnaatntt	gctgggaaat	ttttcctccc	ctaaatntt	tc	772

<210> 12

<211> 751

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(751)

<223> n = A,T,C or G

<400> 12

gccccaatte	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatacaaa	60
agctgattga	agcaaccctc	tacttttttg	tcgtgagcct	tttgcttggt	gcaggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagtanggtg	agtcctcaaa	atccgtatag	ttggtgaagc	cacagcactt	gagccctttc	240
atgggtggtg	tccacacttg	agtgaagtct	tccctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	ggaagtgtct	agccattgtg	gtgtacacca	aggcgaccac	360
agcagctgcn	acctcagcaa	tgaagatgan	gaggangatg	aagaagaacg	tcncgagggc	420
acacttgctc	tcagtcttan	caccatanca	gcccntgaaa	accaananca	aagaccacna	480
cnccggctgc	gatgaagaaa	tnaccccncg	ttgacaaact	tgcatggcac	tggganccac	540
agtggcccn	aaaatcttca	aaaaggatgc	cccactnatt	gaccccccaa	atgcccactg	600
ccaacagggg	ctgccccacn	cncnnaacga	tganccnatt	gnacaagatc	tncntggtct	660
tnatnaacnt	gaacctgcn	tngtggctcc	tgttcaggnc	cnnggcctga	cttctnaann	720
aangaactcn	gaagncccc	cngganann	g			751

<210> 13

<211> 729

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(729)

<223> n = A,T,C or G

<400> 13
gagccaggcg tccctctgcc tgcccaactca gtggcaacac ccgggagctg ttttgcctt 60
tgtggancct cagcagtncc ctctttcaga actcantgcc aaganccctg aacaggagcc 120
accatgcagt gcttcagctt cattaagacc atgatgatcc tcttcaattt gctcatcttt 180
ctgtgtggtg cagccctggt ggcagtgggc atctgggtgt caatcgatgg ggcacccctt 240
ctgaagatct tcgggccact gtcgtccagt gccatgcagt ttgtcaacgt gggctacttc 300
ctcatcgag ccggcggtgt ggtcttagct ctaggtttcc tgggtgcta tgggtgctaag 360
actgagagca agtgtgccct cgtgacgttc ttcttcatcc tctctctcat cttcattgct 420
gaggttgcaa tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttctgacgt 480
tgctggtaat gcctgccatc aanaaaagat tatgggttcc caggaanact tcaactcaagt 540
gttggaaacac caccatgaaa gggctcaagt gctgtggctt cnnccaacta tacggatttt 600
gaagantcac ctacttcaaa gaaaanagt cctttccccc atttctgttg caattgacaa 660
acgtcccaa cacagccaat tgaaaacctg caccacaacc aaangggctc ccaaccanaa 720
attnaaggg 729

<210> 14
<211> 816
<212> DNA
<213> Homo sapien
<220>
<221> misc_feature
<222> (1)...(816)
<223> n = A,T,C or G

<400> 14
tgctcttctt caaagtgtgt cttgttgcca taacaaccac cataggtaaa gcgggagcag 60
tgttcgctga aggggttgta gtaccagcgc gggatgctct ccttgagag tctgtgtct 120
ggcagggtcca cgcagtggcc ttgttactg gggaaatgga tgcgctggag ctctgcaaa 180
ccactcgtgt atttttcaca ggcagcctcg tccgacgcgt cggggcagtt gggggtgtct 240
tcacactcca ggaaactgtc natgcagcag ccattgctgc agcggaactg ggtgggtgta 300
cangtgccag agcacactgg atggcgctt tccatgnan gggccctgng ggaaagtccc 360
tganccecan anctgcctct caaangcccc accttgaca ccccgacagg ctagaatgga 420
atcttcttcc cgaaaggtag ttnttcttgt tgcccaancc anccccntaa acaaactctt 480
gcanatctgc tccngggggg tcntantacc anctgaggaa aagaacccca ggcngcgaac 540
caancttgtt tggatncgaa gcnataatct nctnttctgc ttggtggaca gcaccantna 600
ctgtnnanct ttagncntg gtcctcntgg gttgnncttg aacctaatcn ccnntcaact 660
gggacaaggt aantngccnt cctttnaatt ccnancntn ccccttggtt tggggttttn 720
cncnctcta cccagaaan nccgtgttcc ccccaacta ggggccnaaa ccnntnttc 780
cacaaccctn cccacccac gggttcngnt ggttng 816

<210> 15
<211> 783
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(783)
<223> n = A,T,C or G

<400> 15
ccaaggcctg ggcaggcata nacttgaagg tacaacccca ggaaccctg gtgctgaagg 60
atgtggaaaa cacagattgg cgcctactgc ggggtgacac ggatgtcagg gtagagagga 120
aagacccaaa ccagggtggaa ctgtggggac tcaaggaang cacctacctg ttccagctga 180
cagtactag ctacagaccac ccagaggaca cggccaacgt cacagtcaact gtgctgtcca 240
ccaagcagac agaagactac tgcctcgcat ccaacaangt gggtcgctgc cggggctctt 300
tcccacgctg gtactatgac cccacggagc agatctgcaa gagtttctgt tatggaggct 360

gcttgggcaa	caagaacaac	taccttcggg	aagaagagt	cattctancc	tgtcnggggtg	420
tgcaagggtg	gcctttgana	ngcanctctg	gggtcangc	gactttcccc	cagggcccct	480
ccatggaaag	gcgccatcca	ntgttctctg	gcacctgtca	gcccacccag	ttccgctgca	540
ncaatggctg	ctgcatcnac	antttcctng	aattgtgaca	acacccccca	ntgcccccaa	600
ccctcccaac	aaagcttccc	tgttnaaaaa	tacnccantt	ggcttttnac	aaacnccccg	660
cncctccntt	ttccccntn	aacaaagggc	nctngcnttt	gaactgccc	aaccnnggaa	720
tctnccnngg	aaaaantncc	ccccctgggt	cctnnaancc	cctccncnaa	anctncccc	780
ccc						783

<210> 16

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (801)

<223> n = A,T,C or G

<400> 16

gccccaatc	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatacaaa	60
agctgattga	agcaaccctc	tacttttttg	tctgtagcct	tttgcttggt	gcaggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagtagggtg	agtcctcaaa	atccgtatag	ttggtgaagc	cacagcactt	gagccctttc	240
atggtgggtg	tccacacttg	agtgaagtct	tcttgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	gaagtgtcga	gccattgtgg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgctct	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
ccngctgcga	atgaaagaaa	ntaccacagt	tgacaaaactg	catggccact	ggacgacagt	540
tggccccaan	atcttcagaa	aagggatgcc	ccatcgattg	aacacccana	tgcccactgc	600
cnacagggct	gcncncncn	gaaagaatga	gccattgaag	aaggatcntc	ntggtcttaa	660
tgaactgaaa	ccntgcatgg	tggccctgtg	tcagggtctc	tggcagtga	ttctganaaa	720
aagggaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

<210> 17

<211> 740

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (740)

<223> n = A,T,C or G

<400> 17

gtgagagcca	ggcgtccctc	tgcctgceca	ctcagtggca	acacccggga	gctgttttgt	60
cctttgtgga	gcctcagcag	ttccctcttt	cagaactcac	tgccaagagc	cctgaacagg	120
agccaccatg	cagtgtttca	gcttcattaa	gaccatgatg	atcctcttca	atttgctcat	180
ctttctgtgt	ggtgcagccc	tgttggcagt	gggcactctg	gtgtcaatcg	atggggcatc	240
ctttctgaag	atcttcgggc	cactgtcgtc	cagtggccatg	cagtttgtca	acgtgggcta	300
cttccctcatc	gcagccggcg	ttgtgggtctt	tgtctttggt	ttcctgggct	gctatgggtgc	360
taagacggag	agcaagtgtg	ccctcgtgac	gttctttctt	atcctcctcc	tcattcttcat	420
tgctgaagtt	gcagctgctg	tggtcgctt	ggtgtacacc	acaatggctg	aaccattcct	480
gacgttgctg	gtantgcctg	ccatcaanaa	agattatggg	ttcccaggaa	aaattcactc	540
aantntggaa	caccnccatg	aaaagggctc	caatttctgn	tggttcccc	aactataccg	600
gaattttgaa	agantcnccc	tacttccaaa	aaaaaanant	tgcctttncc	cccnttctgt	660
tgcaatgaaa	acntcccaan	acngccaatn	aaaacctgcc	cnnncaaaaa	ggntcncaaa	720

caaaaaaant nnaagggttn

740

<210> 18
 <211> 802
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(802)
 <223> n = A,T,C or G

<400> 18
 ccgctggttg cgctggtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca 60
 caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg 120
 ggatacactt tacttttagca gccagggtga caactgagag gtgtcgaagc ttattcttct 180
 gagcctctgt tagtggagga agattccggg cttcagctaa gtatgcagcg tatgtcccat 240
 aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa 300
 cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat 360
 ggatgagtgt ggccagcgtt gcccccttgg ccgacttggc taggagcaga aattgctcct 420
 gggttctgcc tgtcaccttc acttccgcac tcatcactgc actgagtgtg ggggacttgg 480
 gctcaggatg tccagagacg tggttccgcc ccctcnctta atgacaccgn ccanncaacc 540
 gtcggctccc gccgantgng ttcgctcgtnc ctgggtcagg gtctgctggc cinctacttgc 600
 aancttcgtc nggccccatg aattcaccnc accggaactn gtangatcca ctntttctat 660
 aaccggncgc caccgcnnnt ggaactccac tcttnttnc tttacttgag ggtaaggtc 720
 acccttnncg ttaccttggt ccaaacntn ccntgtgtcg anatngtnaa tcnggncna 780
 tnccancnc atangaagcc ng 802

<210> 19
 <211> 731
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(731)
 <223> n = A,T,C or G

<400> 19
 cnaagcttcc aggtnacggg ccgcnaancc tgaccnagg tancanaang cagnncggg 60
 gagcccaccg tcacngngng gngtctttat nggagggggc ggagccacat cnetggacnt 120
 cntgacccca actcccnc ncncantgca gtgatgagtg cagaactgaa ggtnacgtgg 180
 caggaacca gancaaannc tgctccntc caagtcggcn nagggggcgg ggctggccac 240
 gcncatcctt cnagtgtgtn aaagcccn cctgtctact tgtttggaga acngcnnga 300
 catgcccagn gttanataac nggcnagag tnannttgcc tctcccttcc ggtgcgcan 360
 cgngtntgct tagnggacat aacctgacta cttaactgaa ccnngaate tncncctt 420
 ccactaagct cagaacaaaa aacttcgaca ccactcantt gtcacctgnc tgctcaagta 480
 aagtgtaccc catncccaat gtntgctnga ngctctgncc tgcnttangt tcggtcctgg 540
 gaagacctat caattnaagc tatgtttctg actgcctctt gtcctctgna acaancnacc 600
 cnnnntcca aggggggggnc ggcccccaat ccccccaacc ntnaattnan ttancccn 660
 cccccnggc cggcctttta cnancntcnn nnaacnggna aaaccnnngc ttncccaac 720
 nnaatecncc t 731

<210> 20
 <211> 754
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (754)

<223> n = A,T,C or G

<400> 20

tttttttttt	tttttttttt	taaaaaacc	ctccattnaa	tgnaaaacttc	cgaaattgtc	60
caaccccctc	ntccaaatnn	ccntttccgg	gnnggggttc	caaacccaan	ttanntttgg	120
annttaaatt	aaatnttntt	tgngngnna	anccnaatgt	nangaaagtt	naaccanta	180
tnancttnaa	tncttgga	ccngtngntt	ccaaaaatnt	ttaaccctta	antccctccg	240
aaatngttna	nggaaaacc	aantttctnt	aagggtgttt	gaaggntnaa	tnaaaanccc	300
nnccaattgt	tttngccac	gcctgaatta	attggnttcc	gntgttttcc	nttaaaanaa	360
ggnnancccc	ggttantnaa	tcccccnnc	cccaattata	ccganttttt	ttngaattgg	420
gancccnccg	gaattaacgg	ggnnntccc	tnttgggggg	cnggnncccc	ccccntccgg	480
ggttngggnc	aggncnnaat	tgtttaaggg	tccgaaaaat	ccctccnaga	aaaaaanctc	540
ccaggntgag	nntnggggtt	cccccccc	cangggccct	ctcgnaaggt	tgggggttgg	600
ggggcctggg	attttntttc	ccctnttnc	cccccccc	ccnggganag	agggtngngt	660
tttgntcnnc	ggccccnccn	aaganctttn	ccganttnan	ttaaatccnt	gcctnggcga	720
agtccttgn	agggtntaaan	ggccccctnn	cggg			754

<210> 21

<211> 755

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (755)

<223> n = A,T,C or G

<400> 21

atcancccat	gacccnaac	nngggaccnc	tcanceggnc	nnncnaccnc	cggccnatca	60
ngtgnagnnc	actncnnttn	natcacnccc	cnccnactac	gcccncnanc	cnagcnccta	120
nncanatncc	actganngcg	cgangtngan	ngagaaanct	nataccanag	ncaccanacn	180
ccagctgtcc	nanaangcct	nnnatacngg	nnnatccaat	ntgnancctc	cnaagtattn	240
nncnncan	gattttcctn	anccgattac	ccntncccc	tanccctcc	cccccaacna	300
cgaaggcnct	ggncnnaagg	nngcgncc	ccgctagntc	cccncaagt	cncncncta	360
aactcancn	nattacnccg	ttcntgagta	tcactccccg	aatctcacc	tactcaactc	420
aaaaanaten	gatacaaaat	aatncaagcc	tgnttatnac	actntgactg	ggtctctatt	480
ttagnngtcc	ntnaancntc	ctaatacttc	cagctcncct	tcnccaattt	ccnaanggct	540
ctttcngaca	gcatnttttg	gttcccnntt	gggttcttan	ngaattgccc	ttcntngaac	600
gggtcntct	tttccctcgg	ttancctggn	ttcnncggc	cagttattat	ttcccntttt	660
aaattcntnc	cntttanttt	tggcnttcna	aacccccggc	cttgaaaacg	gccccctggt	720
aaaaggttgt	tttganaaaa	tttttgtttt	gttcc			755

<210> 22

<211> 849

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (849)

<223> n = A,T,C or G

<400> 22

tttttttttt	tttttangtg	tngtcgtgca	ggtagaggct	tactacaant	gtgaanacgt	60
acgctnggan	taangcgacc	cgantttctag	ganncnccct	aaaatcanac	tgtgaagatn	120

atcctgnnna	cggaanggtc	accggnggat	nttgetaggg	tgncnctec	cannncnttn	180
cataactcng	nggccctgcc	caccaccttc	ggcgggccng	ngnccgggcc	cgggtcattn	240
gnnttaacn	cactnngcna	neggtttccn	nccecnncng	accnnggcga	tccgggggtnc	300
tctgtcttcc	cctgnagncn	anaaantggg	ccnccggncce	ctttaccctt	nnacaagcca	360
engccteta	nccnengccc	cccctccant	nnnggggact	gccnanngt	cgttntctng	420
nnaccccnnn	gggtncctcg	gttgctcgant	cnaccgnang	ccanggattc	cnaaggaagg	480
tgcgttnttg	gcccctaccc	ttcgtctnccg	nnaccccttc	cgcacnanga	nccgtctccg	540
cncnccngng	cctnccctcg	caacacccgc	ntctntcngt	ncggnnnccc	ccccaccgcg	600
ncctctcncc	ngnccgnancn	ctcncnccn	gtctcannca	ccaccccgcc	cgccnagggc	660
ntcanccacn	ggngacnng	nagcncntc	gcncgcgcgn	gcgncnccct	cgccnagaa	720
ctnctcngg	ccantnncgc	tcaancnna	cnaaacgcgc	ctgcgcggcc	cgnagcgncc	780
ncctcncga	gtctcccgcn	cttcnacc	angnttccn	cgaggacacn	nnaccccgcc	840
nnccangcg						849

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

gcgcaaaacta	tacttcgctc	gnactcgtgc	gcctcgtctc	tcttttcttc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatanan	aagntcganc	agtccaaact	gantaacaca	120
cacacnncan	aganaaatcc	netgccttcc	anagtanaen	attgaacnng	agaaccangc	180
nggcgaatcg	taatnaggcg	tgcgcgcgca	atntgtcncc	gtttattntn	ccagctcnc	240
ctnccnacc	tactcttccn	nagctgtcnn	acccctngtn	cgnaccccc	naggctggga	300
tgcgggtttn	nntgaccng	cnnccctcc	ccccctccat	nacganccn	ccgcaccacc	360
nanngcncc	nccecgntct	cttcgcncn	ctgtctctn	ccctgtngc	ctggcncngn	420
accgcattga	ccctcgcenn	ctnccngaaa	ncgnanacgt	ccgggttggn	annapcgtg	480
tgggnnngcg	tctgcncgc	gttccttccn	ncncttcca	ccatcttct	tacngggct	540
ccnccctc	tcnnncacn	cctgggacgc	ntctctncc	ccccctnac	tccccctt	600
cgncgtgncc	cgccccacc	ntcatttnca	nacgntctc	acaannncct	ggntnctcc	660
cnancngncc	gtcancnag	ggaaggngg	ggnnccnntg	nttgacgttg	ngngangtc	720
cgaanantcc	tcnccntcan	cctaccctt	cgggcgntct	ctcngttncc	aacttancaa	780
ntctcccccg	ngngcncntc	tcagcctcnc	ccncccnct	ctctgcantg	tnctctgctc	840
tnaccnntac	gantnttcgn	cncctcttt	cc			872

<210> 24

<211> 815

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(815)

<223> n = A,T,C or G

<400> 24

gcatgcaagc	ttgagtattc	tatagngtca	cctaaatanc	ttggcntaat	catggctnta	60
netgncttcc	tgtgtcaaat	gtatacnaen	tanatatgaa	tctnatntga	caagannnga	120
tctntcatta	gtaacaantg	tnntgtccat	cctgtcngan	canattccca	tnnattnccn	180
cgcattcncn	gencantatn	taatngggaa	ntcnntnnnn	ncacnncat	ctatctncc	240
gcncctgac	tggnagagat	ggatnantt	tnntntgacc	nacatgttca	tcttggattn	300
aananccecc	cgcnngccac	cgggtngnng	cnagcnnct	ccaagacctc	ctgtggaggt	360

aacctgcgtc	aganncatca	aacntgggaa	acccgcnncc	angtnnaagt	ngnnncanan	420
gateccgtcc	aggnttnacc	atcccttcnc	agcgccccct	ttngtgcctt	anagnnagc	480
gtgtccnanc	cnctcaacat	ganacgcgcc	agnccanccg	caattnggca	caatgtcgnc	540
gaaccccccta	gggggantna	tncaaanccc	caggattgtc	cncncangaa	atcccncanc	600
cccnccctac	ccncttttg	gacngtgacc	aantcccgga	gtncagtc	ggcngnctc	660
ccccaccggt	nncntgggg	gggtgaanct	cngnntcanc	cngnccgaggn	ntcgnaagga	720
accggnccctn	ggncgaanng	ancnntcnga	agngccnctn	cgtataaccc	cccctcncca	780
nccnacngnt	agntcccccc	cngggtnccg	aangg			815

<210> 25

<211> 775

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(775)

<223> n = A,T,C or G

<400> 25

ccgagatgtc	tcgctccgtg	gccttagctg	tgctcgcgt	actctctctt	tctggcctgg	60
aggctatcca	gcgtactcca	aagattcagg	tttactcacg	tcatccagca	gagaatggaa	120
agtcaaattt	cctgaattgc	tatgtgtctg	ggtttcatcc	atccgacatt	gaanttgc	180
tactgaagaa	tgganagaga	attgaaaaag	tggagcattc	agacttgtct	ttcagcaagg	240
actggtcttt	ctatctctng	tactacactg	aattcacccc	cactgaaaaa	gatgagtatg	300
cctgccgtgt	gaaccatgtg	actttgtcac	agcccaagat	agttaagtgg	gatcgagaca	360
tgtaagcagn	cnnatggaa	gtttgaagat	gccgcatttg	gattggatga	attccaaatt	420
ctgcttgctt	gcnttttaat	antgatatgc	ntatacaccc	taccctttat	gnccccaat	480
tgtaggggtt	acatnantgt	tcnctntngga	catgatcttc	ctttataant	ccnccnttcg	540
aattgcccgt	cncnngttn	ngaattgttc	cnaaccacg	gttggtcccc	ccaggtcncc	600
tcttacggaa	gggcctgggc	cnctttncaa	ggttggggga	accnaaaatt	tcnctnttgc	660
cncccncca	cnntcttng	nncncanttt	ggaacccttc	cnattccctt	tggectcna	720
nccttnncta	anaaaacttn	aaancgtngc	naaanntttt	acttcccccc	ttacc	775

<210> 26

<211> 820

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(820)

<223> n = A,T,C or G

<400> 26

anattantac	agtgtaatct	tttcccagag	gtgtgtanag	ggaacggggc	ctagaggcat	60
cccanagata	ncttatanca	acagtgtctt	gaccaagagc	tgctgggcac	atttctgca	120
gaaaagggtg	cgggtcccat	cactcctcct	ctcccatagc	catcccagag	gggtgagtag	180
ccatcangcc	ttcggtggga	gggagtcang	gaaacaacan	accacagagc	anacagacca	240
ntgatgacca	tgggcgggag	cgagcctctt	ccctgnaccg	gggtggcana	nganagccta	300
nctgagggggt	cacactataa	acgttaacga	ccnagatnan	cacctgtctc	aagtgcaccc	360
ttcctacctg	acnaccagng	accnnaact	gcngcctggg	gacagcnctg	ggancagcta	420
acnnagcact	cacctgcccc	cccatggccg	tnccgntccc	tggtcctgnc	aagggaagct	480
ccctgttggga	attncgggga	naccaaggga	nccccctcct	ccanctgtga	aggaaaaann	540
gatggaattt	tncccttcg	gcnntcccc	tcttcttcta	cacgccccct	nntactcttc	600
tccctctntt	ntcctgnenc	acttttnacc	ccnnnatctt	ccttnattga	tcggannctn	660
ganattccac	tnncgcctnc	cntcnatcng	naanacnaaa	nactntctna	ccnggggat	720
gggnncctcg	ntcatectct	ctttttcnct	accnccnntt	ctttgcctct	ccttngatca	780

tccaacntc gntggcctn ccccccnntc tcctttncce

820

<210> 27

<211> 818

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(818)

<223> n = A,T,C or G

<400> 27

tctgggtgat	ggcctcttcc	tcctcagggg	cctctgactg	ctctgggcca	aagaatctct	60
tgttttcttct	ccgagcccca	ggcagcgggtg	attcagccct	gcccacctg	attctgatga	120
ctgcggtatgc	tgtgacggac	ccaaggggca	aataggggtcc	caggggtccag	ggagggggcgc	180
ctgctgagca	cttccgcccc	tcacctgccc	cagccccctgc	catgagctct	gggctgggtc	240
tccgctcca	gggttctgct	cttccangca	ngccancaaag	tggcgctggg	ccacactggc	300
ttcttctgccc	cccttccctg	gctctganc	tctgtcttcc	tgctctgtgc	angcnccttg	360
gatctcagtt	tccttctctc	anngaactct	gtttctgann	tcttcantta	actntgantt	420
tatnaccnan	tggncgtgnc	tgctcnaactt	taatgggccc	gaccggctaa	tccttccctc	480
ntcccttccc	anttcnnnna	accngcttnc	cntctctccc	ccntancccg	ccnggggaanc	540
ctcctttgcc	ctnaccangg	gccnnnaccc	ccctnnctn	ggggggcnnng	gtnnctnccn	600
ctgntnnccc	cnetcncnnt	tnctctgtcc	cnnnncnccn	nngcannctc	nngtcccn	660
tnctctctcn	ngtntcgnaa	ngtctcctn	tnnnnnngcn	ngtntnctn	tcctctctc	720
cnnntgnang	tnnttnnnnc	ncngnncccc	nnnnnnnnnn	ngnnntnnn	tctnccngc	780
ccnncccc	ngnattaagg	cctcnnctc	ccggccnc			818

<210> 28

<211> 731

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 28

aggaagggcg	gagggatatt	gtangggatt	gagggatagg	agnataangg	gggaggtgtg	60
tcccaacatg	anggtgnngt	tctcttttga	angaggggtg	ngtttttann	ccnggtgggt	120
gattnaaccc	cattgtatgg	agnnaaagg	tttnagggat	ttttcggtc	ttatcagtat	180
ntanattcct	gtnaatcgga	aaatnatntt	tcnncnggaa	aatnttgctc	ccatccgnaa	240
attntcccc	ggtagtgc	nttngggggg	cngccangtt	tcccaggctg	ctanaatcgt	300
actaaagntt	naagtgggan	tncaaatgaa	aacctnncc	agagnatccn	taccgcactg	360
tnnnctnct	tcgcccctng	actctgcnn	agcccaatac	ccnngngnat	gtcncnccn	420
nnngcgncc	tgaaannnn	tcngggctnn	gancatcang	gggtttcgca	tcaaaagcnn	480
cgtttncat	naaggcactt	tnccctcatc	caaccnctng	ccctcnncca	tttngccgtc	540
nggttncct	acgtntntng	cncctnnntn	ganattttnc	ccgcctnggg	naancctcct	600
gnaatgggta	gggncttntc	ttttnacn	gnggtntact	aatcnnctnc	acgcntnctt	660
tctcnacccc	cccccttttt	caatcccan	ggcnaatggg	gtctccccnn	cgangggggg	720
nnnccann	c					731

<210> 29

<211> 822

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(822)
 <223> n = A,T,C or G

<400> 29
 actagtccag tgtggtggaa ttccattgtg ttgggggnnc ttctatgant antnttagat 60
 cgctcanacc tcacancctc ccnacnangc ctataangaa nannaataga nctgtncnnt 120
 atntntacnc tcatanncct cnnnacccac tccctcttaa cccntactgt gcctatngcn 180
 tnnctantct ntgccgcctn cnanccaccn gtggggccnac cncnngnatt ctcnatctcc 240
 tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn 300
 tccatnantt annntaacta ccaactgacnt ngactttenc atnanctcct aatttgaatc 360
 tactctgact cccacngcct annnattagc anctcccccc nacnatntct caaccaaadc 420
 ntcaacaacc tatctantcy ttcnccaacc nttncctccg atccccnnac aacccccctc 480
 ccaaataccc nccacctgac nccaaaccn caccatcccg gcaagccnan ggncatttan 540
 ccaactggaat cacnatngga naaaaaaac ccnaactctc tanencnnat ctccctaana 600
 aatnctcctn naatttactn ncantnccat caancccaen tgaaacnnaa cccctgtttt 660
 tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc cccccnctnc 720
 ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaaggcna anannntccg 780
 canatcctat cccttanttn ggggnccctt nccnggggcc cc 822

<210> 30
 <211> 787
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(787)
 <223> n = A,T,C or G

<400> 30
 eggccgcctg ctctggcaca tgccctcctga atggcatcaa aagtgatgga ctgcccattg 60
 ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt 120
 gtctgcagga tttgatgtct gaagtcgtgg agtgtggctt ggagctcctc atctacatna 180
 gctggaagcc ctggagggcc tctctcgcca gcctccccct tctctccacg ctctccangg 240
 acaccagggg ctccaggcag cccattattc ccagnangac atgggtgtttc tccacgcgga 300
 cccatggggc ctgnaaggcc aggggtctct ttgacaccat ctctcccgtc ctgctggca 360
 ggccgtggga tccactantt ctanaacggn cgccaccncc gtgggagctc cagcttttgt 420
 tcccnttaat gaaggttaat tgcnccgttg gcgtaatcat nggtcanaac tntttcctgt 480
 gtgaaattgt tntccccctc ncnatccnc ncnacatacn aacccggaan cataaagtgt 540
 taaagcctgg gggtnccctn nngaataaac tnaactcaat taattgcgtt ggctcatggc 600
 ccgcttccn ttcnngaaaa ctgtctctcc ctgcnttnnt gaatcgcca cccccnggg 660
 aaaagcggtt tgcnttttng ggggntcctt ccncttcccc cctcnctaan cctnccgct 720
 cggctgttnc nggtngcggg gaangggnat nnnctccnc naagggggng agnnngntat 780
 ccccaa 787

<210> 31
 <211> 799
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(799)
 <223> n = A,T,C or G

<400> 31

tttttttttt	tttttttggc	gatgctactg	tttaattgca	ggaggtgggg	gtgtgtgtac	60
catgtaccag	ggctattaga	agcaagaagg	aaggagggag	ggcagagcgc	cctgctgagc	120
aacaaaggac	tcctgcagcc	ttctctgtct	gtctcttggc	gcaggcacat	ggggaggcct	180
cccgccagggt	ggggggccacc	agtccagggg	tgggagcact	acanggggtg	ggagtgggtg	240
gtggctggtn	cnaatggcct	gncacanatc	cctacgattc	ttgacacctg	gatttcacca	300
ggggaccttc	tggtctccca	nggnaacttc	ntnnatctcn	aaagaacaca	actgtttctt	360
cngcanttct	ggctgttcat	ggaaagcaca	ggtgtccnat	ttnggctggg	acttggtaca	420
tatgggtccg	gcccacctct	cccntcnaan	aagtaattca	ccccccccc	ccntctnttg	480
cctgggccc	taantaccca	caccggaact	canttantta	ttcatcttng	gntgggcttg	540
ntnatcnccn	cctgaangcg	ccaagttgaa	aggccacgcc	gtncnccnctc	cccatagnan	600
nttttnnct	canctaagtc	ccccccnggc	aacnatccaa	ccccccccc	tgggggcccc	660
agcccanggc	ccccgntctg	ggnnnccngn	cncgnantcc	ccaggntctc	ccantcngnc	720
ccnnngcncc	cccgccagca	gaacanaagg	ntngagccnc	cgcannnnnn	nggtnnncac	780
ctcgccccc	ccnnccgng					799

<210> 32

<211> 789

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(789)

<223> n = A,T,C or G

<400> 32

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
ttttncnag	ggcagggtta	ttgacaacct	cncgggacac	aancaggctg	gggacaggac	120
ggeaacaggc	tccggcggcg	gcggcgggcg	ccctacctgc	ggtaccaa	ntgcagcctc	180
cgctcccgt	tgatnttct	ctgcagctgc	aggatgccnt	aaaacagggc	ctcgcccntn	240
ggtgggcacc	ctgggatttn	aatttccacg	ggcacaatgc	ggtcgcancc	cctcaccacc	300
nattaggaat	agtggtnnta	ccnccnccg	ttggcncact	ccccntggaa	accacttntc	360
gcggctcccg	catctggtct	taaaccttgc	aaacnctggg	gccctctttt	tggttantnt	420
nccngccaca	atcatnactc	agactggcnc	gggctggccc	caaaaaancn	ccccaaaacc	480
ggncatgtc	ttnnccgggt	tgctgcnatn	tncatcacct	cccgggcnca	ncaggncaac	540
ccaaaagtct	ttgnggccc	caaaaaanct	ccggggggnc	ccagtttcaa	caaagtcac	600
ccccctggcc	cccaaatect	ccccccgntt	nctgggtttg	ggaaccacg	cctctnnctt	660
tggnnggcaa	gntggntccc	ccttcggggc	cccgggtggg	ccnctctaa	ngaaaacncc	720
ntcctnnnca	ccatccccc	nngnnacgnc	tancaangna	tccctttttt	tanaaacggg	780
ccccccnccg						789

<210> 33

<211> 793

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(793)

<223> n = A,T,C or G

<400> 33

gacagaacat	gttggatggt	ggagcacctt	tctatacgac	ttacaggaca	gcagatgggg	60
aattcatggc	tggtggagca	atanaacccc	agttctacga	gctgctgac	aaaggacttg	120
gactaaagtc	tgatgaactt	cccaatcaga	tgagcatgga	tgattggcca	gaaatgaana	180
agaagtttgc	agatgtattt	gcaaagaaga	cgaaggcaga	gtggtgtcaa	atctttgacg	240
gcacagatgc	ctgtgtgact	ccggttctga	cttttgagga	ggttggtcat	catgatcaca	300
acaangaacg	gggctcgttt	atcaccantg	aggagcagga	cgtgagcccc	cgccttcgac	360

ctctgctgtt	aaacacccca	gcatccctt	ctttcaaaag	ggatccacta	cttctagagc	420
ggncgccacc	gcggtggagc	tccagctttt	gttcccttta	gtgaggggta	attgcgcgct	480
tggcgtaatc	atggtcatan	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaatttt	aaagcctggn	ggtngcctaa	tgantgaact	600
nactcacatt	aattggcttt	gcgctcactg	cccgctttcc	agtcoggaaa	acctgtcctt	660
gccagctgcc	nttaatgaat	cnggccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgcncttccc	gctttctcgc	ttectgaant	ccttcccccc	ggtctttcgg	cttgcggcna	780
acggtatcna	cct					793

<210> 34
 <211> 756
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(756)
 <223> n = A,T,C or G

gccgcgaccg	gcatgtacga	gcaactcaag	ggcgagtggg	accgtaaaag	ccccaatctt	60
ancaagtgcg	gggaanagct	gggtcgactc	aagctagttc	ttctggagct	caacttcttg	120
ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccgtga	catactggag	180
atcgggggccc	aatggagcat	cctacgcaan	gacatccctc	ccttcgagcg	ctacatggcc	240
cagctcaaat	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttcctg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtcctgga	gcaatactga	tgganggcag	ctaccncaaa	gtnttctctg	ccnagggtaa	480
catcccccg	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcaggggatg	540
aaaatcgcn	ggttgtcca	gaaaggctnc	aanaanatcc	ttttcncctga	aggcccccg	600
atncnctagt	nctagaatcg	gcccgccatc	gcggtgganc	ctccaacctt	tcgttnccct	660
ttactgaggg	ttnattgccg	cccttggcgt	tatcatggtc	acncnngttn	cctgtgttga	720
aattnttaac	cccccaaat	tccacgcna	cattng			756

<210> 35
 <211> 834
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(834)
 <223> n = A,T,C or G

ggggatctct	anactnacct	gnatgcatgg	ttgtcggtgt	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggtc	gctgtnttta	agttgctcag	tctgccgtca	120
tagtcagaca	cncctctggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcnng	gctgtctgct	cggtgaactc	gatgacnang	ggcagctggg	tgtgtntgat	240
aaantccanc	angttctcct	tggtgacctc	cccttcaaag	ttgttcgggc	cttcatcaaa	300
cttctnnaan	angannancc	canctttgtc	gagctggnat	ttgganaaca	cgctactggt	360
ggaaactgat	cccaaattgg	atgtcatcca	tcgcctctgc	tgccctgcaa	aaacttgctt	420
ggcncaaatc	cgactcccn	tccttgaaag	aagccnatca	cacccccctc	cctggactcc	480
nncaangact	ctnccgctnc	cccntccnng	cagggttggg	ggcannccgg	gcccntgcgc	540
ttcttcagcc	agttcaacna	nttcatcagc	ccctctgcc	gctgttntat	tccttggggg	600
ggaanccgtc	tctcccttcc	tgaannaact	ttgaccgtng	gaatagccgc	gcntcncnt	660
acntnctggg	ccgggttcaa	antccctccn	ttgncnntcn	cctcgggcca	ttctggattt	720
nccnaacttt	tctcttcccc	cncnccnccg	ngtttggntt	tttcatnggg	ccccaactct	780

gctnttggcc antcccctgg gggcntntan cccccctnt ggtcccntng ggcc

834

<210> 36
 <211> 814
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(814)
 <223> n = A,T,C or G

<400> 36
 cggncgcttt ccngcgcgc cccgtttcca tgacnaagge tcccttcang ttaaatacnn 60
 cctagnaaac attaatgggt tgctctacta atacatcata cnaaccagta agcctgcca 120
 naacgccaac tcagccatt cctaccaaag gaagaaagge tggctctctc accccctgta 180
 ggaaaggcct gccttgtaag acaccacaat nccgctgaat ctnaagtctt gtgttttact 240
 aatggaaaaa aaaaataaac aanaggtttt gttctcatgg ctgcccaccg cagcctggca 300
 ctaaaacanc ccagcgtca cttctgcttg ganaaatatt ctttgcctt ttggacatca 360
 ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc 420
 antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc 480
 aggggagctg ntttncagtg gatctgccaa anantaccn tatcatcnnt gaataaaaag 540
 gcccctgaac ganatgcttc cancanctt taagacccat aatcctngaa ccatgggtgcc 600
 ctcccggtct gatccnaaag gaatgttctt gggteccant ccttcctttg ttncttacgt 660
 tgtnttggac cntgtctngn atnaccaan tganatcccc ngaagcacc tncctctggc 720
 atttganttt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcncnnaan 780
 ggngaactca agaaggtctn ngaaaaacca cncn 814

<210> 37
 <211> 760
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(760)
 <223> n = A,T,C or G

<400> 37
 gcatgctgct ctctctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg 60
 gcgcagtgtt cgctgaagg gttgtagtac cagcgcggga tgctctcctt gcagagtcct 120
 gtgtctggca ggtccacgca atgcccttg tctactggga aatggatgag ctggagctcg 180
 tcnaanccac tcgtgtattt ttcacangca gcctcctccg aagctccgg gcagttgggg 240
 gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt 300
 gggctgacag gtgccagaac aactggatn ggcctttcca tggaagggcc tgggggaaat 360
 cncctnancc caaactgcct ctcaaaggcc acctgcaca ccccgacagg ctagaaatgc 420
 actcttcttc ccaaaggtag ttgttcttgt tgcccaagca nctccanca aacaaaaanc 480
 ttgcaaaatc tgctccgtgg gggcatnnn taccanggtt ggggaaanaa acccgcngn 540
 ganccnctt gtttgaatgc naaggnaata atcctcctgt cttgcttggg tggaaagca 600
 caattgaact gttaacnttg ggccnggtt cncnnggtg gtctgaaact aatcacgctc 660
 actggaaaaa ggtangtgc ttccttgaat tcccaaantt cccctngntt tgggtntttt 720
 ctctctncc ctaaaaatcg tnttcccccc ccntanggcg 760

<210> 38
 <211> 724
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(724)

<223> n = A,T,C or G

<400> 38

tttttttttt	tttttttttt	tttttttttt	tttttaaaaa	ccccctccat	tgaatgaaaa	60
cttcnnaaat	tgtccaaccc	cctcnnccaa	atnccattt	cggggggggg	gttccaaacc	120
caaattaatt	ttgganttta	aattaaatnt	tnattngggg	aanaanccaa	atgtnaagaa	180
aatttaaccc	attatnaact	taaatacctn	gaaacccntg	gnttccaaaa	atttttaacc	240
cttaaattcc	tccgaaattg	ntaanggaaa	accaaattcn	cctaaggctn	tttgaagggt	300
ngattttaac	ccccttnant	tnttttnacc	cnngnctnaa	ntatttngnt	tccggtgttt	360
tcctnttaan	cntnggtaac	tcccgnataa	gaannnccct	aanccaatta	aaccgaattt	420
tttttgaatt	ggaaattccn	ngggaattna	cgggggtttt	tcccnttttg	gggccatncc	480
cccnctttcg	gggtttgggn	ntaggttgaa	tttttnnang	ncccaaaaaa	ncccccaana	540
aaaaaaactcc	caagnnttaa	ttngaattnc	ccccttccca	ggccttttgg	gaaaggnggg	600
ttntggggg	ccngggantt	enttcccccn	ttncncccc	ccccccnggt	aaanggttat	660
ngnnttgggt	ttttgggccc	cttnanggac	cttccggatn	gaaattaaat	ccccgggncg	720
gccg						724

<210> 39

<211> 751

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(751)

<223> n = A,T,C or G

<400> 39

tttttttttt	tttttctttg	ctcacattta	atttttattt	tgattttttt	taatgctgca	60
caacacaata	tttatttcat	ttgtttcttt	tatttcattt	tatttgtttg	ctgctgctgt	120
tttatttatt	tttactgaaa	gtgagaggga	acttttggtg	ccttttttcc	tttttctgta	180
ggccgcctta	agcttttctaa	atttggaaca	tctaagcaag	ctgaanggaa	aaggggggtt	240
cgcaaaatca	ctcgggggaa	nggaaagggt	gctttgttaa	tcatgcccta	tggtgggtga	300
ttaactgctt	gtacaattac	ntttcacttt	taattaattg	tgctnaangc	tttaattana	360
cttggggggt	ccctccccan	accaaccccn	ctgacaaaaa	gtgccngccc	tcaaatnatg	420
tcccggcnnt	cnttgaaaca	cacngcngaa	ngttctcatt	ntcccnccnc	caggtnaaaa	480
tgaagggtta	ccatntttta	cnccacctcc	acntggcnnn	gcctgaatcc	tcnaaaancn	540
ccctcaancn	aattnctnng	ccccgggtcnc	gcntnngtcc	cncccggggt	cggggaantn	600
cacccccnga	anncnntnnc	naacnaaatt	ccgaaaatat	tcccnntcnc	tcaattcccc	660
cnnagactnt	cctcnncnan	cncaattttc	ttttnttcac	gaacncgnnc	cnnaaaatgn	720
nnnnnccttc	cncnngtccn	naatcnccan	c			751

<210> 40

<211> 753

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(753)

<223> n = A,T,C or G

<400> 40

gtgggtatttt	ctgtaagatc	aggtgttcc	ccctcgtagg	tttagaggaa	acacccctcat	60
agatgaaaac	ccccccgaga	cagcagcact	gcaactgcca	agcagccggg	gtaggagggg	120

cgccctatgc	acagctgggc	ccttgagaca	gcagggcttc	gatgtcaggc	tcgatgtcaa	180
tggtctggaa	gcggcggctg	tacctgcgta	ggggcacacc	gtcagggccc	accaggaact	240
tctcaaagtt	ccaggcaacn	tcgttgcgac	acaccggaga	ccaggtgatn	agcttgggggt	300
cggtcataa	cgcggtggcg	tcgtcgctgg	gagctggcag	ggcctcccgc	aggaaggcna	360
ataaaaggtg	cgcccccgca	ccgttcanc	cgcacttctc	naanaccatg	angttgggct	420
cnaaccacc	accannccgg	acttccttga	nggaattccc	aatctcttcc	gntcttgggc	480
ttctnctgat	gccctanctg	gttgcctcng	atgccaanca	nccccaancc	ccggggtcct	540
aaanacccn	cctcctcctt	tcactctgggt	tntntcccc	ggaccttggt	tcctctcaag	600
gganccata	tctcnaccan	tactcacnt	nccccccnt	gnnaccanc	cttctanngn	660
ttccncccg	ncctctggcc	ontcaaan	gcttnacna	cctgggtctg	ccttcccccc	720
tnccctatct	gnacccn	tttgtctcan	tnt			753

<210> 41

<211> 341

<212> DNA

<213> Homo sapien

<400> 41

actatatcca	tcacaacaga	catgcttcat	cccatagact	tcttgacata	gcttcaaagt	60
agtgaaccca	tccttgattt	atatacatat	atgttctcag	tattttggga	gcctttccac	120
ttctttaaac	cttggtcatt	atgaacactg	aaaataggaa	tttgtgaaga	gttaaaaagt	180
tatagcttgt	ttacgtagta	agtttttgaa	gtctacattc	aatccagaca	cttagttgag	240
tggttaaactg	tgatttttaa	aaaatatcat	ttgagaatat	tctttcagag	gtattttcat	300
ttttactttt	tgattaattg	tgttttatat	attagggtag	t		341

<210> 42

<211> 101

<212> DNA

<213> Homo sapien

<400> 42

acttactgaa	tttagttctg	tgctcttcc	tatttagtgt	tgtatcataa	atactttgat	60
gtttcaaaca	ttctaaataa	ataattttca	gtggcttcat	a		101

<210> 43

<211> 305

<212> DNA

<213> Homo sapien

<400> 43

acatctttgt	tacagtctaa	gatgtgttct	taaatcacca	ttccttctg	gtcctcacc	60
tccaggggtg	tctcacactg	taattagagc	tattgaggag	tctttacagc	aaattaagat	120
tcagatgcct	tgctaagtct	agagttctag	agttatgttt	cagaaagtct	aagaaaccca	180
cctcttgaga	ggtcagtaaa	gaggacttaa	tatttcatat	ctacaaaatg	accacaggat	240
tgatacaga	acgagagtta	tcctggataa	ctcagagctg	agtacctgcc	cgggggcccgc	300
tcgaa						305

<210> 44

<211> 852

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(852)

<223> n = A,T,C or G

<400> 44

```

acataaaatat cagagaaaag tagtctttga aatattttacg tccaggagtt ctttgtttct 60
gattatttgg tgtgtgtttt gggttgtgtc caaagtattg gcagcttcag ttttcatttt 120
ctctccatcc tegggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct 180
ccagaatttc tctttttag taatatctca tagctcggtc gagcttttca taggtcatgc 240
tgctgttgtt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga 300
agacgccctc agatcgggtc tcccatttta ttaatcctgg gttcttgtct gggttcaaga 360
ggatgtcgcg gatgaattcc cataagttag tccctctcgg gttgtgtctt ttggtgtggc 420
acttggcagg ggggtcttgc tcttttttca tatcagggtga ctctgcaaca ggaaggtgac 480
tggtggttgc catggagatc tgagcccgcc agaaagtatt gctgtccaac aaatctactg 540
tgctaccata gttggtgtca tataaatagt tctngtcttt ccagggtgtc atgatggaag 600
gctcagtttg ttcagtcttg acaatgacat tgtgtgtgga ctggaacagg tcaactactgc 660
actggccggt ccacttcaga tgctgcaagt tgctgtagag gagntgcccc gccgtccctg 720
ccgcccgggt gaactcctgc aaactcatgc tgcaaagggt ctcgccgttg atgtcgaact 780
cntggaaagg gatacaattg gcatccagct ggttgggtgc caggagggtga tggagccact 840
cccacacctg gt 852

```

<210> 45
 <211> 234
 <212> DNA
 <213> Homo sapien

```

<400> 45
acaacagacc cttgctcgct aacgaacctca tgctcatcaa gttggacgaa tccgtgtccg 60
agtctgacac catccggagc atcagcattg cttcgcagtg cctaccgcg ggaactcctt 120
gcctcgtttc tggctggggg ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg 180
tgaacgtgtc ggtggtgtct gaggaggtct gcagtaagct ctatgacccg ctgt 234

```

<210> 46
 <211> 590
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (590)
 <223> n = A,T,C or G

```

<400> 46
actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta 60
attttagatgc aatatttttg agattacaga gtttttagtaa ttaccaatta cacagttaaa 120
aagaagataa tatattccaa gcanatacaa aatatctaata gaaagatcaa ggcaggaaaa 180
tgantataac taattgacaa tggaaaatca attttaatgt gaattgcaca ttatccttta 240
aaagctttca aaanaaanaa ttattgcagt ctanttaatt caaacagtgt taaatggtat 300
caggataaan aactgaaggg canaaagaat taattttcac ttcattgtaac ncacccanat 360
ttacaatggc ttaaattgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc 420
tggtctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag 480
ggctcctggt atatccacaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct 540
gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt 590

```

<210> 47
 <211> 774
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (774)
 <223> n = A,T,C or G

<400> 47

acaagggggc	ataatgaagg	agtggggana	gatttttaaag	aaggaaaaaa	aacgaggccc	60
tgaacagaat	tttcctgnac	aacggggcctt	caaaataatt	ttcttgggga	ggttcaagac	120
gctttactgc	ttgaaactta	aatggatgtg	ggacanaatt	ttctgtaatg	accctgaggg	180
cattacagac	gggactctgg	gaggaaggat	aaacagaaag	gggacaaagg	ctaateccaa	240
aacatcaaag	aaaggaaggt	ggcgtcatac	ctcccagcct	acacagttct	ccagggtctct	300
cctcatccct	ggaggacgac	agtggaggaa	caactgacca	tgcccccagg	ctcctgtgtg	360
ctggctcctg	gtcttcagcc	cccagctctg	gaagcccacc	ctctgctgat	cctgcgtggc	420
ccacactcct	tgaacacaca	tccccaggtt	atattcctgg	acatggctga	acctcctatt	480
cctacttccg	agatgccttg	ctccctgcag	cctgtcaaaa	tcccactcac	cctccaaacc	540
acggcatggg	aagcctttct	gacttgcttg	attactccag	catcttgga	caatccctga	600
ttccccactc	cttagaggca	agataggggtg	gttaagagta	gggctggacc	acttggagcc	660
aggctgctgg	cttcaaattn	tggctcattt	acgagctatg	ggaccttggg	caagtnatct	720
tcactttctat	gggcntcatt	ttgtttctacc	tgcaaaatgg	gggataataa	tagt	774

<210> 48

<211> 124

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(124)

<223> n = A,T,C or G

<400> 48

canaaattga	aattttataa	aaaggcattt	ttctcttata	tccataaaat	gatataattt	60
ttgcaantat	anaaatgtgt	cataaattat	aatgttcctt	aattacagct	caacgcaact	120
tggt						124

<210> 49

<211> 147

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(147)

<223> n = A,T,C or G

<400> 49

gccgatgcta	ctattttatt	gcaggaggtg	ggggtgtttt	tattattctc	tcaacagctt	60
tgtggctaca	ggtggtgtct	gactgcatna	aaaanttttt	tacgggtgat	tgcaaaaatt	120
ttagggcacc	catatcccaa	gcantgt				147

<210> 50

<211> 107

<212> DNA

<213> Homo sapien

<400> 50

acattaaatt	aataaaagga	ctgttggggt	tctgctaaaa	cacatggctt	gatatattgc	60
atggtttgag	gttaggagga	gttaggcata	tgttttggga	gaggggt		107

<210> 51

<211> 204

<212> DNA

<213> Homo sapien

<400> 51

gtcctaggaa	gtctagggga	cacacgactc	tgggggtcacg	gggccgacac	acttgcacgg	60
cgggaaggaa	aggcagagaa	gtgacaccgt	caggggggaaa	tgacagaaag	gaaaatcaag	120
gccttgcaag	gtcagaaagg	ggactcaggg	cttcaccac	agccctgccc	cacttggcca	180
cctccctttt	gggaccagca	atgt				204

<210> 52

<211> 491

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (491)

<223> n = A,T,C or G

<400> 52

acaaagataa	catttatctt	ataacaaaaa	tttgatagtt	ttaaagggtta	gtattgtgta	60
gggtattttc	caaaagacta	aagagataac	tcaggtaaaa	agttagaaat	gtataaaaaca	120
ccatcagaca	ggttttttaa	aaacaacata	ttacaaaatt	agacaatcat	ccttaaaaaa	180
aaaacttctt	gtatcaattt	cttttgttca	aaatgactga	cttaantatt	tttaaatttt	240
tcanaaacac	ttcctcaaaa	attttcaana	tggtagcttt	canatgtnc	ctcagtccca	300
atgttgctca	gataaataaa	tctcgtgaga	acttaccacc	caccacaagc	tttctggggc	360
atgcaacagt	gtcttttctt	tnctttttct	tttttttttt	ttacaggcac	agaaactcat	420
caattttatt	tggataacaa	agggtctcca	aatttatattg	aaaaataaat	ccaagttaat	480
atcactcttg	t					491

<210> 53

<211> 484

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (484)

<223> n = A,T,C or G

<400> 53

acataattta	gcagggctaa	ttaccataag	atgctattta	ttaanaggtn	tatgatctga	60
gtattaacag	ttgctgaagt	ttgggtattt	tatgcagcat	tttctttttg	ctttgataac	120
actacagaac	ccttaaggac	actgaaaatt	agtaagtaaa	gttcagaaac	attagctgct	180
caatcaaadc	tctacataac	actatagtaa	ttaaaacggt	aaaaaaaaag	gttgaaatct	240
gcactagtat	anaccgctcc	tgtcaggata	anactgcttt	ggaacagaaa	gggaaaaanc	300
agctttgant	ttctttgtgc	tgatangagg	aaaggctgaa	ttaccttggt	gcctctccct	360
aatgattggc	aggtcnggta	aatnccaaaa	catattccaa	ctcaacactt	cttttccnec	420
tancctgant	ctgtgtattc	caggancagg	cggatggaat	gggccagccc	ncggatgttc	480
cant						484

<210> 54

<211> 151

<212> DNA

<213> Homo sapien

<400> 54

actaaacctc	gtgcttgtga	actccataca	gaaaacgggtg	ccatccctga	acacggctgg	60
ccactgggta	tactgctgac	aaccgcaaca	acaaaaacac	aaatcccttg	cactggctag	120

tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55
 <211> 91
 <212> DNA
 <213> Homo sapien

<400> 55
 acctggettg tctccgggtg gttcccggeg ccccccacgg tccccagaac ggacactttc 60
 gccctccagt ggatactcga gccaaagtgg t 91

<210> 56
 <211> 133
 <212> DNA
 <213> Homo sapien

<400> 56
 ggcggtatgtg cgttgggttat atacaaatat gtcattttat gtaagggact tgagtatact 60
 tggatttttg gtatctgtgg gttgggggga cggtcagga accaatatccc catggatacc 120
 aagggaacaac tgt 133

<210> 57
 <211> 147
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(147)
 <223> n = A,T,C or G

<400> 57
 actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60
 gactgggagc tgagcccttc cctttgcgcc tgcctcagag gattgttgcc gacntgcana 120
 tctcantggg ctggatncat gcagggt 147

<210> 58
 <211> 198
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(198)
 <223> n = A,T,C or G

<400> 58
 acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60
 tgattacata catttatect ttaaaaaaga tgtaaactctt aatttttatg ccatctatta 120
 atttaccat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180
 ttgacttcta agtttggt 198

<210> 59
 <211> 330
 <212> DNA
 <213> Homo sapien

<400> 59

acaacaaatg ggttgtagg aagtcttatac agcaaaactg gtgatggcta ctgaaaagat	60
ccattgaaaa ttatcattaa tgatttttaa tgacaagtta tcaaaaactc actcaatttt	120
cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa	180
tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagaccag	240
cagaaggaaat ctattttatc acatggatct cegtctgtgc tcaaaatacc taatgatatt	300
tttcgtcttt attggacttc tttgaagagt	330

<210> 60
 <211> 175
 <212> DNA
 <213> Homo sapien

<400> 60	
accgtgggtg ccttctacat tcttgacggc tcttcacca acatctggtt ctacttcggc	60
gtcgtgggtg ctttctcttt catctcctc cagctgggtg tgctcatcga ctttgcgac	120
tcttggaacc agcgggtggc gggcaaggcc gaggagtgcg attcccgtgc ctggt	175

<210> 61
 <211> 154
 <212> DNA
 <213> Homo sapien

<400> 61	
accccacttt tctcctgtg agcagctctg acttctcact gctacatgat gaggtgagt	60
ggttggttgc cttcaacagt atcctccct ttcggatct gctgagccgg acagcagtgc	120
tggactgcac agccccggg ctccacattg ctgt	154

<210> 62
 <211> 30
 <212> DNA
 <213> Homo sapien

<400> 62	
cgctcgagcc ctatagttag tctgtattaga	30

<210> 63
 <211> 89
 <212> DNA
 <213> Homo sapien

<400> 63	
acaagtcatt tcagcaccct ttgtcttca aaactgacca tcttttatat ttaatgttc	60
ctgtatgaat aaaaatggtt atgtcaagt	89

<210> 64
 <211> 97
 <212> DNA
 <213> Homo sapien

<400> 64	
accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag	60
aatcagtga tccaggattg gtccttggat ctgggggt	97

<210> 65
 <211> 377
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(377)

<223> n = A,T,C or G

<400> 65

acaacaanaa ntccttctt taggcactg atggaaacct ggaacccct tttgatggca	60
gcatggcgct ctaggccttg acacagcggc tggggtttgg gctntcccaa accgcacacc	120
ccaaccctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggt	180
tcggtcataa natgaaatcc caanggggac agaggctcagt agaggaagct caatgagaaa	240
ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg	300
tgggggtgaa ctaccccan gaggaatcat gcctgggcga tgcaanggtg ccaacaggag	360
gggcgggagg agcatgt	377

<210> 66

<211> 305

<212> DNA

<213> Homo sapien

<400> 66

acgcctttcc ctcagaattc agggaagaga ctgtcgctg ccttcctccg ttgttgctg	60
agaacccgtg tgcccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg	120
aggaactaac tgcaccctgg tcctctcccc agtccccagt tcaccctcca tccctcacct	180
tcctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt	240
ttatatattt ttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac	300
tgttt	305

<210> 67

<211> 385

<212> DNA

<213> Homo sapien

<400> 67

actacacaca ctccacttgc cttgtgaga cactttgtcc cagcacttta ggaatgctga	60
ggtcggacca gccacatctc atgtgcaaga ttgcccagca gacatcaggc ctgagagttc	120
cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc	180
tgtgctgtgc tggagattca cttttgagag agttctctc tgagacctga tcttttagagg	240
ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg	300
cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac	360
catagtttct gtgctagtgg accgt	385

<210> 68

<211> 73

<212> DNA

<213> Homo sapien

<400> 68

acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa	60
gtttttttta tgg	73

<210> 69

<211> 536

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(536)

<223> n = A,T,C or G

<400> 69

actagtcacag	tgtggtggaa	ttccattgtg	ttgggggctc	tcaccctcct	ctcctgcagc	60
tccagctttg	tgctctgcct	ctgaggagac	catggcccag	catctgagta	ccctgctgct	120
cctgctggcc	accctagctg	tgccctggc	ctggagcccc	aaggaggagg	ataggataat	180
cccgggtggc	atctataacg	cagacctcaa	tgatgagtgg	gtacagcgtg	cccttcactt	240
cgccatcagc	gagtataaca	aggccaccaa	agatgactac	tacagacgtc	cgctgcgggt	300
actaagagcc	aggcaacaga	ccgttggggg	ggtgaattac	ttcttcgacg	tagagggtggg	360
ccgaaccata	tgtaccaagt	cccagcccaa	cttggacacc	tgtgccttcc	atgaacagcc	420
agaactgcag	aagaacagt	tgtgctcttt	cgagatctac	gaagttccct	ggggagaaca	480
gaangtcctt	gggtgaaatc	caggtgtcaa	gaaatcctan	ggatctgttg	ccaggc	536

<210> 70

<211> 477

<212> DNA

<213> Homo sapien

<400> 70

atgaccccta	acagggggccc	tctcagccct	cctaattgacc	tccggcctag	ccatgtgatt	60
tcacttccac	tccataacgc	tcctcatact	aggcctacta	accaacacac	taaccatata	120
ccaatgatgg	cgcgatgtaa	cacgagaaag	cacataccaa	ggccaccaca	caccacctgt	180
ccaaaaaggc	cttcgatacg	ggataatcct	atttattacc	tcagaagttt	ttttcttcgc	240
agggattttt	ctgagccttt	taccactcca	gcctagcccc	taccccccaa	ctaggagggc	300
actggccccc	aacaggcatc	accccgctaa	atcccttaga	agtccctctc	ctaaacacat	360
ccgtattact	cgcctcagga	gtatcaatca	cctgagctca	ccatagtcta	atagaaaaca	420
accgaaacca	aattattcaa	agcactgctt	attacaattt	tactgggtct	ctattttt	477

<210> 71

<211> 533

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(533)

<223> n = A,T,C or G

<400> 71

agagctatag	gtacagtgtg	atctcagctt	tgcaaacaca	ttttctacat	agatagtact	60
agggtattaat	agatatgtaa	agaaagaaat	cacaccatta	ataatggtaa	gattggttta	120
tgtgattttta	gtggattttt	tggcaccctt	atatatgttt	tccaaacttt	cagcagtgat	180
attattttcca	taacttaaaa	agtgagtttg	aaaaagaaaa	tctccagcaa	gcattctcatt	240
taaataaagg	tttgtcatct	ttaaaaatac	agcaatatgt	gactttttta	aaaagctgtc	300
aaatagggtgt	gaccctacta	ataattatta	gaaatacatt	taaaaacatc	gagtacctca	360
agtcagtttg	ccttgaaaaa	tatcaaatat	aactcttaga	gaaatgtaca	taaaagaatg	420
cttcgtaatt	ttggagtang	aggttccctc	ctcaattttg	tattttttaa	aagtacatgg	480
taaaaaaaaa	aattcacaac	agtatataag	gctgtaaaaa	gaagaattct	gcc	533

<210> 72

<211> 511

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(511)

<223> n = A,T,C or G

<400> 72

tattacggaa	aaacacacca	cataattcaa	ctancaaaga	anactgcttc	agggcgtgta	60
aatgaaagg	cttccaggca	gttatctgat	taaagaacac	taaaagaggg	acaaggctaa	120
aagccgcagg	atgtctacac	tatancaggc	gctatttggg	ttggctggag	gagctgtgga	180
aaacatggan	agattggtgc	tgganacgc	cgtggctatt	cctcattgtt	attacanagt	240
gaggttctct	gtgtgcccac	tggtttgaaa	accgttctnc	aataatgata	gaatagtaca	300
cacatgagaa	ctgaaatggc	ccaaacccag	aaagaaagcc	caactagatc	ctcagaanac	360
gcttctaggg	acaataaccg	atgaagaaaa	gatggcctcc	ttgtgcccc	gtctgttatg	420
atttctctcc	attgcagcna	naaacccgtt	cttctaagca	aacncagggtg	atgatggcna	480
aaatacacc	cctcttgaag	naccnggagg	a			511

<210> 73

<211> 499

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(499)

<223> n = A,T,C or G

<400> 73

cagtgccagc	actggtgcca	gtaccagtag	caataacagt	gccagtgcc	gtgccagcac	60
cagtgggtggc	ttcagtgtctg	gtgccagcct	gaccgccact	ctcacatttg	ggctcttcgc	120
tggccttggt	ggagctgggtg	ccagcaccag	tggcagctct	ggtgccctgtg	gtttctccta	180
caagtgagat	tttagatatt	gttaatcctg	ccagtctttc	tcttcaagcc	aggggtgcac	240
ctcagaaacc	tactcaacac	agcactctag	gcagccacta	tcaatcaatt	gaagttgaca	300
ctctgcatta	aatctatttg	ccatttctga	aaaaaaaaaa	aaaaaaaggg	cggccgctcg	360
antctagagg	gcccgtttta	acccgctgat	cagcctcgac	tgtgccttct	anttgccagc	420
catctgttgt	ttgccccctcc	cccgntgcct	tccttgaccc	tggaaagtgc	cactcccact	480
gtcctttcct	aantaaaaat					499

<210> 74

<211> 537

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(537)

<223> n = A,T,C or G

<400> 74

tttcatagga	gaacacactg	aggagatact	tgaagaattt	ggattcagcc	gcgaagagat	60
ttatcagctt	aactcagata	aatcattga	aagtaataag	gtaaaagcta	gtctctaact	120
tccaggccca	cggctcaagt	gaatttgaat	actgcattta	cagtgtagag	taacacataa	180
cattgtatgc	atggaaacat	ggaggaacag	tattacagtg	tcctaccact	ctaatcaaga	240
aaagaattac	agactctgat	tctacagtga	tgattgaatt	ctaaaaatgg	taatcattag	300
ggctttttgat	ttataanact	ttgggtactt	atactaaatt	atggtagtta	tactgccttc	360
cagtttgctt	gatataattg	ttgatattaa	gattcttgac	ttatattttg	aatgggttct	420
actgaaaaan	gaatgatata	ttcttgaaga	catcgatata	catttattta	cactcttgat	480
tctacaatgt	agaaaatgaa	ggaaatgccc	caaattgtat	ggtgataaaa	gtccccgt	537

<210> 75

<211> 467

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(467)
 <223> n = A,T,C or G

<400> 75
 caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60
 tgcattattac acgtacctcc tctgtctcct caagtagtgt ggtctatatt gccatcatca 120
 cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
 tggcacaagg aggccatctt ttctctcatg gttattgtcc ctagaagcgt cttctgagga 240
 tctagttggg ctttctttct gggtttgggc catttcantt ctcattgtgt tactattcta 300
 tcattattgt ataacgggtt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360
 caatgaggaa tagccacggg gatctccagc accaaatctc tccatgttnt tccagagctc 420
 ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

<210> 76
 <211> 400
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(400)
 <223> n = A,T,C or G

<400> 76
 aagctgacag cattcggggc gagatgtctc gctccgtggc cttagctgtg ctgcgcgtac 60
 tctctctttc tggcctggag gctatccagc gtactccaaa gattcagggt tactcacgtc 120
 atccagcaga gaattgaaag tcaaatttcc tgaattgcta tgtgtctggg ttctatccat 180
 ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagtg gagcattcag 240
 acttgtcttt cagcaaggac tgggtctttc atctcttgta ctacactgaa ttcaccccca 300
 ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360
 ttnagtggga tcganacatg taagcagcan catgggaggt 400

<210> 77
 <211> 248
 <212> DNA
 <213> Homo sapien

<400> 77
 ctggagtgcc ttggtgtttc aagccccctgc aggaagcaga atgcaccttc tgaggcacct 60
 ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgtgtc 120
 caggcactgt tcattctcagc ttttctgtcc ctttgtctcc ggcaagcgtc tctgtgaaa 180
 gttcatatct ggagcctgat gtcttaacga ataaaggctc catgtctcac ccgaaaaaaa 240
 aaaaaaaa 248

<210> 78
 <211> 201
 <212> DNA
 <213> Homo sapien

<400> 78
 actagtccag tgtggtggaa ttccattgtg ttggggcccaa cacaatggct acctttaaca 60
 tcacccagac ccgcacctgc ccgtgcccc aagctgtgtc aacgacagta tgatgcttac 120
 tctgtactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataaatgcct 180
 gatttaaaaa aaaaaaaaaa a 201

<210> 79
 <211> 552
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (552)
 <223> n = A,T,C or G

<400> 79
 tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg 60
 tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt 120
 cctctttctt ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag 180
 tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt 240
 atgcaagtta gtaattactc agggttaact aaattacttt aatatgctgt tgaacctact 300
 ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga 360
 taatattcta tgtttctaaa gttgggctat acataaanta tnaagaaata tggaatttta 420
 ttcccaggaa tatgggggtt atttatgaat antaccggg anagaagttt tgantnaaac 480
 cngttttggt taatacgtta atatgtcctn aatnaacaag gcntgactta tttccaaaaa 540
 aaaaaaaaaa aa 552

<210> 80
 <211> 476
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (476)
 <223> n = A,T,C or G

<400> 80
 acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga 60
 ggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120
 cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt 180
 gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtacta 240
 aggttaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac 300
 tcttctaagt cctcttccag cctcactttg agtcctcctt gggggttgat aggaantntc 360
 tcttggtttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat 420
 gctgaaaaaa ttaaaatgtt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81
 <211> 232
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (232)
 <223> n = A,T,C or G

<400> 81
 tttttttttg tatgcntcn ctgtgnggtt attgttgctg ccaccctgga ggagcccagt 60
 ttcttctgta tctttctttt ctgggggagc ttcttggtc tgccttcca tttccagcct 120
 ctcatcccca tcttgactt ttgctagggg tggaggcgct ttcttggtag cccctcagag 180
 actcagtcag cggaataag tcttaggggt ggggggtgtg gcaagccggc ct 232

<210> 82
<211> 383
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 82
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactgggtgcc 60
agtaccagta ccaataacat gccagtgcc gtgccagcac cagtgggtggc ttcagtgctg 120
gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggt ggagctgggt 180
ccagcaccag tggcagctct ggtgcctgtg gtttctccta caagtgagat tttagatatt 240
gttaatectg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac 300
agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360
ccatttcaaa aaaaaaaaaa aaa 383

<210> 83
<211> 494
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(494)
<223> n = A,T,C or G

<400> 83
accgaattgg gaccgtggc ttataagcga tcatgtctc cagtattacc tcaacgagca 60
gggagatcga gtctatacgc tgaagaaatt tgacccgatg ggacaacaga cctgctcagc 120
ccatcctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa 180
acgcttcaag gtgctcatga cccagcaacc gcgcctgtc ctctgagggt ccttaaaactg 240
atgtcttttc tgccacctgt taccctctcg agactccgta accaaactct tcggactgtg 300
agccctgatg cctttttgcc agccatactc tttggcntcc agtctctcgt ggcgattgat 360
tatgcttgtg tgaggcaatc atgggtggcat caccatnaa gggaacacat ttganttttt 420
tttcncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta 480
aaaaaaaaaa aaaa 494

<210> 84
<211> 380
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

<400> 84
gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca 60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120
gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg 180
gcacaccctc ctgggggccca ggcgggcacc tgcgtctccc agtatgccaa ctggctgggtg 240
gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctgggtcac ttgctcattg 300
ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
agcgttnccg cctcatccgg 380

<210> 85
 <211> 481
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(481)
 <223> n = A,T,C or G

<400> 85
 gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggctctcgc ttcataccgc 60
 tnccatcgtc atactgtagg tttgccacca cctcctgcat cttggggcgg ctaatatcca 120
 ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg 180
 tgtgaaagga tctccagaag gagggtctga tcttccccac acttttgatg actttattga 240
 gtcgattctg catgtccagc aggaggttgt accagctctc tgacagttag gtcaccagcc 300
 ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgggggggt gnagtctcac 360
 ccagattctg cattaccaga naggcgtggc aaaaganatt gacaactcgc ccaggngaa 420
 aaagaacacc tcttgaagt gctngccgt cctcgtcctt tggtggnngc gcntnccttt 480
 t 481

<210> 86
 <211> 472
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(472)
 <223> n = A,T,C or G

<400> 86
 aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt 60
 acttgaaaaa gcaacttnaa gcctggacac tggattataa attcacaata tgcaacactt 120
 taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg 180
 ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct ttttttttga 240
 cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcactttctt 300
 catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg 360
 atatntgagc ggaagantag cctttctact tcaccagaca caactccttt catattggga 420
 tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg 472

<210> 87
 <211> 413
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(413)
 <223> n = A,T,C or G

<400> 87
 agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaatth ttgtgtgcgtg 60
 tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttgta aaagcttatg 120
 cctcttttgt atctatatct gtgaaagttt taatgatctg ccataatgct ttggggacct 180
 ttgtcttctg tgtaaagtgt actagagaaa acacctatnt tatgagtcaa tctagttngt 240
 tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg 300

ggggacaaaag aaaagcanaa ctgaacatna gaaacaattn cctggtgaga aattncataa 360
acagaaattg ggtngtatat tgaaanannng catcattnaa acgttttttt ttt 413

<210> 88
<211> 448
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(448)
<223> n = A,T,C or G

<400> 88
cgcagcgggt cctctctatc tagctccagc ctctcgctg cccactccc cgcgtcccgc 60
gtcctagccn accatggccg ggcccctgcg cgcccgcgtg ctctgctgg ccatcctggc 120
cgtggccctg gccgtgagcc ccgcgcccg ctcagctccc ggcaagccgc cgcgctgggt 180
gggaggccca tggacccgc gtggaagaag aaggtgtgcg gcgtgactg gactttgccg 240
tcggcnanta caacaaacc gcaacnactt ttaccnagcn cgcgtgcag gttgtgccgc 300
cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctg gccaaacnng 360
tttaccagaa ccnagccaat tngaacaatt nccccctcat aacagcccct tttaaaaagg 420
gaancantcc tgnctctttc caaat ttt 448

<210> 89
<211> 463
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(463)
<223> n = A,T,C or G

<400> 89
gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca 60
gtagtgattc tgccaaagt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc 120
agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt 180
ctcagtgaca agttntttct gatgcgaagt tctnattcca gtgttttagt cctttgcac 240
tttnatgtn agacttgcc ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg 300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn 360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn 420
aattcnana anttcagntn tcatacaaca naacngganc ccc 463

<210> 90
<211> 400
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(400)
<223> n = A,T,C or G

<400> 90
agggattgaa ggtctntnt actgtcggac tgttcancca ccaactctac aagttgctgt 60
cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaat 120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttccact 180
tcctttgtta agacttcac tggtaaagtc ttaagttttg tagaaaggaa ttttaattgct 240

cgttctctaa caatgtcctc tccttgaagt atttggctga acaaccacc tnaagtcctt	300
ttgtgcatcc attttaata tacttaata ggcattggtg cactagggtta aattctgcaa	360
gagtcactcg tctgcaaaag ttgcgttagt atatctgcca	400

<210> 91
 <211> 480
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(480)
 <223> n = A,T,C or G

<400> 91	
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact	60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac	120
atgcctcttt gactaccgtg tgccagtgtt ggtgattctc acacacctcc nnccgctctt	180
tgtggaaaaa ctggcacttg nctggaacta gcaagacatc acttacaatc tcaccacaga	240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt	300
tgtcaatact aaccgctgg tttgcctcca tcacatttgt gatctgtagc tctggataca	360
tctcctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctgtt	420
ngatcagggt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa	480

<210> 92
 <211> 477
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(477)
 <223> n = A,T,C or G

<400> 92	
atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact	60
ggtcccgtg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcctt	120
cccacgcagg cagcagcggg gccggccaat gaactccact cgtggcttgg ggttgacggt	180
taantgcagg aagaggctga ccacctcgcg gtccaccagg atgcccgaact gtgcgggacc	240
tgcagcgaat ctctctgatg gtcattgagc ggaagcgaat gangcccagg gccttgccca	300
gaaccttccg cctgttctct ggcgctacct gcagctgctg ccgctnacac tcggcctcgg	360
accagcggac aaacggcgtt gaacagccgc acctcacgga tgcccantgt gtcgcgctcc	420
aggaacggcn ccagcgtgtc caggccaatg tcggtgaanc ctccgcgggt aatggcg	477

<210> 93
 <211> 377
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(377)
 <223> n = A,T,C or G

<400> 93	
gaacggctgg acctgcctc gcatttgtgt gctggcagga ataccttggc aagcagctcc	60
agtccgagca gccccagacc gctgccgcc gaagctaagc ctgcctctgg ccttcccctc	120
cgctcaatg cagaaccant agtgggagca ctgtgtttag agttaagagt gaacactgtn	180

```

tgattttact tgggaatttc ctctgttata tagcttttcc caatgctaata ttccaaacaa 240
caacaacaaa ataacatggt tgctgtttna gttgtataaa agtangtgat tctgtatnta 300
aagaaaatat tactgttaca tatactgctt gcaanttctg tatttattgg tntcttgga 360
ataaatatat tattaata 377

```

```

<210> 94
<211> 495
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(495)
<223> n = A,T,C or G

```

```

<400> 94
ccctttgagg ggtaggggtc cagttcccag tggaagaaac aggccaggag aantgcgtgc 60
cgagctgang cagatttccc acagtgaccc cagagccctg ggctatagtc tctgacctt 120
ccaaggaaag accaccttct ggggacatgg gctggagggc aggacctaga ggcaccaagg 180
gaaggcccca ttccggggct gttccccgag gaggaaggga aggggctctg tgtgcccccc 240
acgaggaana ggccttgant cctgggatca nacacccctt cacgtgtatc cccacacaaa 300
tgcaagctca ccaaggtccc ctctcagtc cttccctaca ccctgaacgg nactggccc 360
acaccaccc agancancca cccgccatgg ggaatgtntc caaggaatcg cngggcaacg 420
tgactctng tcccnnaagg gggcagaatc tccaatagan gganngaacc cttgctnana 480
aaaaaaaaaa aaaaaa 495

```

```

<210> 95
<211> 472
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

```

```

<400> 95
ggttacttgg ttctattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60
cctctggaag ccttgcgag agcggacttt gtaattgttg gagaataact gctgaatttt 120
tagctgtttt gagtgtattc gcaccactgc accacaactc aatatgaaaa ctatttnact 180
tatttattat cttgtgaaaa gtatacaatg aaaattttgt tcatactgta ttatcaagt 240
atgatgaaaa gcaatagata tatattcttt tattatgtnn aattatgatt gccattatta 300
atcggaacaa tgtggagtgt atgttctttt cacagtaata tatgcctttt gtaacttcac 360
ttggttattt tattgtaaat gaattacaaa attcttaatt taagaaaatg gtangttata 420
tttanttcan taatttcttt cttgttttac gtttaattttg aaaagaatgc at 472

```

```

<210> 96
<211> 476
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(476)
<223> n = A,T,C or G

```

```

<400> 96
ctgaagcatt tcttcaaact tntctacttt tgtcattgat acctgtagta agttgacaat 60

```

gtggtgaaat	ttcaaaatta	tatgtaactt	ctactagttt	tactttctcc	cccaagtctt	120
ttttaactca	tgattttttac	acacacaatc	cagaacttat	tatatagcct	ctaagtcttt	180
attcttcaca	gtagatgatg	aaagagtcct	ccagtgtctt	gngcanaatg	ttctagntat	240
agctggatac	atacngtggg	agttctataa	actcatacct	cagtgggact	naaccaaaat	300
tgtgttagtc	tcaattccta	ccacactgag	ggagcctccc	aaatcactat	attcttatct	360
gcaggctactc	ctccagaaaa	acngacaggg	caggcttgca	tgaaaaagtn	acatctgcgt	420
tacaaagtct	atcttctca	nangtctgtn	aaggaacaat	ttaatcttct	agcttt	476

<210> 97

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(479)

<223> n = A,T,C or G

<400> 97

actctttcta	atgctgatat	gatcttgagt	ataagaatgc	atgtgtcact	agaatggata	60
aaataatgct	gcaaacttaa	tgttcttatg	caaaatggaa	cgctaataaa	acacagctta	120
caatcgcaaa	tcaaaactca	caagtgtcca	tctgtttag	atttagtgta	ataagactta	180
gattgtgctc	cttcggatat	gattgtttct	canatcttgg	gcaatnttcc	ttagtcaaat	240
caggctacta	gaattctgtt	attggatatn	tgagagcatg	aaatttttaa	naatacactt	300
gtgattatna	aattaatcac	aaatttcact	tatacctgct	atcagcagct	agaaaaacat	360
ntnnttttta	natcaaagta	ttttgtgttt	ggaantgttn	aatgaaatc	tgaatgtggg	420
ttcnatctta	ttttttcccn	gacnactant	tnctttttta	gggnctattc	tganccatc	479

<210> 98

<211> 461

<212> DNA

<213> Homo sapien

<400> 98

agtgacttgt	cctccaacaa	aacccttga	tcaagtttgt	ggcactgaca	atcagacctt	60
tgctagttcc	tgctatctat	tcgctactaa	atgcagactg	gaggggacca	aaaaggggca	120
tcaactccag	ctggattatt	ttggagcctg	caaactctatt	cctacttgta	cggactttga	180
agtgattcag	tttctctctac	ggatgagaga	ctggctcaag	aatatcctca	tgcagcttta	240
tgaagccact	ctgaacacgc	tggttatcta	gatgagaaca	gagaaataaa	gtcagaaaaat	300
ttacctggag	aaaagaggct	ttggctgggg	accatcccat	tgaaccttct	cttaaggact	360
ttaagaaaaa	ctaccacatg	ttgtgtatcc	tggtgccggc	cgtttatgaa	ctgaccaccc	420
tttggataaa	tcttgacgct	cctgaacttg	ctcctctgcg	a		461

<210> 99

<211> 171

<212> DNA

<213> Homo sapien

<400> 99

gtggcgcgcg	gcagggtgtt	cctcgtagcg	cagggccccc	tcccttcccc	aggcgctcct	60
cggcgccctc	gcgggcccga	ggaggagcgg	ctggcggggtg	gggggagtg	gaccaccct	120
cggtgagaaa	agccttctct	agcgatctga	gaggcggtgcc	ttgggggtac	c	171

<210> 100

<211> 269

<212> DNA

<213> Homo sapien

<400> 100

cggccgcaag	tgcaactcca	gctggggccg	tgccggacgaa	gattctgcc	gcagttggtc	60
cgactgcgac	gacggcggcg	gcgacagtcg	caggtgcagc	gcgggcgcct	ggggtcttgc	120
aaggtgagc	tgacgcgcga	gaggtcgtgt	cacgtccac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccggt	gaagcgggag	gcctcgggga	gcccctcggg	aagggcggcc	240
cgagagatac	gcaggtgcag	gtggccgcc				269

<210> 101

<211> 405

<212> DNA

<213> Homo sapien

<400> 101

tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttatttttga	60
gctagcaagg	taacagggta	gggcatgggt	acatgttcag	gtcaacttcc	ttgtcgtgg	120
ttgattgggt	tgtctttatg	ggggcggggt	ggggtagggg	aaacgaagca	aataacatgg	180
agtgggtgca	ccctccctgt	agaacctggt	tacaaagctt	ggggcagttc	acctgggtctg	240
tgaccgtcat	tttcttgaca	tcaatgttat	tagaagtcag	gatatctttt	agagagtcca	300
ctgttctgga	gggagattag	ggtttcttgc	caaatccaac	aaaatccact	gaaaaagtgt	360
gatgatcagt	acgaataccg	aggcatattc	tcatatcggt	ggcca		405

<210> 102

<211> 470

<212> DNA

<213> Homo sapien

<400> 102

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
ggcacttaat	ccatttttat	ttcaaaatgt	ctacaaattt	aatcccatta	tacggtatatt	120
tcaaaatcta	aattattcaa	attagccaaa	tccttaccaa	ataataccca	aaaatcaaaa	180
atatacttct	ttcagcaaac	ttgttacata	aattaaaaaa	atatatacgg	ctgggtgtttt	240
caaagtacaa	ttatcttaac	actgcaaaca	ttttaaggaa	ctaaaaataa	aaaaaacact	300
ccgcaaagg	ttaaagggaac	aacaaattct	tttacaacac	cattataaaa	atcatatctc	360
aaatcttagg	ggaatatata	cttcacacgg	gatcttaact	tttactcact	ttgtttattt	420
ttttaaacca	ttgtttgggc	ccaacacaat	ggaatcccc	ctggactagt		470

<210> 103

<211> 581

<212> DNA

<213> Homo sapien

<400> 103

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttatttttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaatggaaa	ctgccttaga	tacataatc	ttaggaatta	gcttaaaaac	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaaac	atccaaatc	240
atttttcttg	tctttaaaa	tatctaatot	ttccattttt	tcctattcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	tttctctaaa	360
agggaaaaca	ggaagagaaa	tggcacacaa	aacaaacatt	ttatattcat	atttctacct	420
acgttaataa	aatagcattt	tgtgaagcca	gctcaaaaaga	aggcttagat	ccttttatgt	480
ccatttttagt	cactaaacga	tatcaaagtg	ccagaatgca	aaaggtttgt	gaacatttat	540
tcaaaagcta	atataagata	tttcacatac	tcatctttct	g		581

<210> 104

<211> 578

<212> DNA

<213> Homo sapien

<400> 104

tttttttttt	tttttttttt	tttttctctt	cttttttttt	gaaatgagga	tgcagttttt	60
cactctctag	atagggcatg	aagaaaactc	atctttccag	ctttaaaata	acaatcaaat	120
ctcttatgct	atatcatatt	ttaagttaaa	ctaattgagc	actggcttat	cttctcctga	180
aggaaatctg	ttcattcttc	tcattcatat	agttatatca	agtactacct	tgcattattga	240
gaggtttttc	ttctctattt	acacatatat	ttccatgtga	atttgtatca	aacctttatt	300
ttcatgcaaa	ctagaaaata	atgtttcttt	tgcataagag	aagagaacaa	tatagcatta	360
caaaactgct	caaattgttt	gttaagttat	ccattataat	tagttggcag	gagctaatac	420
aaatcacatt	tacgacagca	ataataaaaac	tgaagtacca	gttaaatatc	caaaataatt	480
aaaggaacat	ttttagcctg	ggtataatta	gctaattcac	tttacaagca	tttattagaa	540
tgaattcaca	tgttattatt	cctagcccaa	cacaatgg			578

<210> 105

<211> 538

<212> DNA

<213> Homo sapien

<400> 105

tttttttttt	tttttcagta	ataatcagaa	caatattttat	tttttatattt	aaaattcata	60
gaaaagtgcc	ttacatttaa	taaaagtttg	tttctcaaag	tgatcagagg	aattagatat	120
gtcttgaaca	ccaatattaa	tttgaggaaa	atacaccaaa	atacattaag	taaattattt	180
aagatcatag	agcttgaag	tgaaaagata	aaatttgacc	tcagaaaactc	tgagcattaa	240
aaatccacta	ttagcaata	aattactatg	gacttcttgc	tttaattttg	tgatgaatat	300
ggggtgtcac	tggtaaacca	acacattctg	aaggatacat	tacttagtga	tagattctta	360
tgtactttgc	taatacgtgg	atatgagttg	acaagtttct	ctttcttcaa	tcttttaagg	420
ggcgagaaat	gaggaagaaa	agaaaaggat	tacgcatact	gttctttcta	tggaaggatt	480
agatatgttt	cctttgccaa	tattaaaaaa	ataataatgt	ttactactag	tgaaaccc	538

<210> 106

<211> 473

<212> DNA

<213> Homo sapien

<400> 106

tttttttttt	tttttttagtc	aagtttctat	ttttattata	attaaagtct	tggtcatttc	60
atttatttagc	tctgcaactt	acatatttaa	attaaagaaa	cgttttagac	aactgtacaa	120
tttataaatg	taagggtgcca	ttattgagta	atatattcct	ccaagagtgg	atgtgtccct	180
tctcccacca	actaatgaac	agcaacatta	gtttaatttt	attagtagat	atacactgct	240
gcaaacgcta	attctcttct	ccatccccat	gtgatattgt	gtatatgtgt	gagttggtag	300
aatgcatac	aatctacaat	caacagcaag	atgaagctag	gctgggcttt	cggtgaaaat	360
agactgtgtc	tgtctgaatc	aaatgatctg	acctatcctc	ggtggcaaga	actcttcgaa	420
cgccttctct	aaaggcgctg	ccacatttgt	ggctctttgc	acttgtttca	aaa	473

<210> 107

<211> 1621

<212> DNA

<213> Homo sapien

<400> 107

cgccatggca	ctgcagggca	tctcggtcat	ggagctgtcc	ggcctggccc	cgggcccgtt	60
ctgtgctatg	gtcctggctg	acttcggggc	gcgtgtggta	cgcgtggacc	ggcccggctc	120
ccgctacgac	gtgagccgct	tgggcccggg	caagcgctcg	ctagtgtgtg	acctgaagca	180
gccgcgggga	gccgcggtgc	tgcggcgctc	gtgcaagcgg	tcggatgtgc	tgetggagcc	240
cttcgcgcgc	ggtgtcatgg	agaaactcca	gctgggccc	gagattctgc	agcgggaaaa	300
tccaaggctt	atttatgcca	ggctgagttg	atttggccag	tcaggaagct	tctgccggtt	360
agctggccac	gatatacaact	atttggcttt	gtcaggtgtt	ctctcaaaaa	ttggcagaag	420
tggtgagaat	ccgtatgccc	cgctgaatct	cctggctgac	tttgcgtgtg	gtggccttat	480
gtgtgcactg	ggcattataa	tggctctttt	tgaccgcaca	cgcactgaca	agggtcaggt	540


```

cattgatgca aatatggtgg aaggaaacagc atattttaagt tcttttctgt ggaaaactca 600
gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatggtg gagcaccttt 660
ctatacgact tacaggacag cagatgggga attcatggct gttggagcaa tagaacccca 720
gttctacgag ctgctgatca aaggacttgg aactaaagtct gatgaacttc ccaatcagat 780
gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac 840
gaaggcagag tgggtgtcaaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac 900
ttttgaggag gttgttcatc atgatacaca caaggaacgg ggctcgttta tcaccagtga 960
ggagcaggac gtgagcccc gccctgcacc tctgctgtta aacaccccag ccateccctc 1020
tttcaaaagg gatcctttca taggagaaca cactgaggag atacttgaag aatttggatt 1080
cagccgcgaa gagattttatc agcttaactc agataaaaatc attgaaagta ataaggtaaa 1140
agctagtctc taacttccag gcccacggct caagtgaatt tgaatactgc atttacagt 1200
tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta 1260
ccactctaata caagaaaaga attacagact ctgattctac agtgaatgatt gaattctaaa 1320
aatggttatc attagggctt ttgatttata aaactttggg tacttatact aaattatggt 1380
agttattctg ccttccagtt tgcttgatat atttgttgat attaagattc ttgacttata 1440
ttttgaatgg gttctagtga aaaaggaatg atatattctt gaagacatcg atatacattt 1500
atttacactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatggtgat 1560
aaaagtcacg tgaacaacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
a 1621

```

<210> 108

<211> 382

<212> PRT

<213> Homo sapien

<400> 108

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1 5 10 15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20 25 30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35 40 45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50 55 60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65 70 75 80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85 90 95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100 105 110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115 120 125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130 135 140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145 150 155 160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165 170 175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180 185 190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195 200 205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210 215 220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225 230 235 240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245 250 255

```

Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
 290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
 355 360 365
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

<210> 109
 <211> 1524
 <212> DNA
 <213> Homo sapien

<400> 109
 ggcacgaggc tgcgccaggc cctgagcgga ggcgggggca gcctcgccag cggggggcccc 60
 gggcctggcc atgcctcact gagccagcgc ctgcgcctct acctcgccga cagctggaac 120
 cagtgcgacc tagtggtctt cacctgcttc ctctgggctg tgggctgccg gctgaccccg 180
 ggtttgtacc acctgggccc cactgtcttc tgcctcgact tcatggtttt cagggtgcgg 240
 ctgcttcaca tcttcacggc caacaaacag ctggggccca agatcgatcat cgtgagcaag 300
 atgatgaagg acgtgttctt ctctctcttc ttctcggcg tgtggctggg agcctatggc 360
 gtggccacgg aggggtcctt gaggccacgg gacagtgaact tcccaagtat cctgcgccgc 420
 gtcttctacc gtccttacct gcagatcttc gggcagattc cccaggagga catggacgtg 480
 gccctcatgg agcacagcaa ctgctcgtcg gagcccggct tctgggcaca cctcctggg 540
 gcccaggcgg gcacatgctt ctcccagtat gccaaactggc tgggtggtgt gctcctcgtc 600
 atcttctcgc tcgtggccaa catctgctg gtcaacttgc tcattgccat gttcagttac 660
 acattcggca aagtacaggc caacagcgat ctctactgga aggcgcagcg ttaccgcctc 720
 atccgggaat tccactctcg gcccgcgctg gcccgcctt ttatcgatcat ctcccacttg 780
 cgctcctcgc tcaggcaatt gtgcaggcga ccccgagacc cccagccgct ctcccggcc 840
 ctcgagcatt tccgggttta ctttcttaag gaagccgagc ggaagctgct aacgtgggaa 900
 tcggtgcata aggagaactt tctgctggca cgcgctaggg acaagcggga gagcgactcc 960
 gagcgtctga agcgcacgtc ccagaagggt gacttggcac tgaaacagct gggacacatc 1020
 cgcgagtacg aacagcgctt gaaagtgtcg gagcgggagg tccagcagtg tagccgcgtc 1080
 ctgggggtggg tggccgaggc cctgagccgc tctgccttgc tgccccagg tgggcccga 1140
 cccctgacc tgcctgggtc caaagactga gccctgctgg cggacttcaa ggagaagccc 1200
 ccacagggga ttttgtcctt agagtaaggc tcatctgggc ctcgccccc gcacctggtg 1260
 gccttgtcct tgaggtgagc cccatgtcca tctggggccac tgtcaggacc accttggga 1320
 gtgtcatcct tacaaccac agcatgccc gctcctccca gaaccagtcc cagcctggga 1380
 ggatcaaggc ctggatccc ggccgttatc catctggagg ctgcagggtc cttggggtaa 1440
 cagggaccac agaccctca cactcacag attcctcaca ctggggaaat aaagccattt 1500
 cagaggaaaa aaaaaaaaaa aaaa 1524

<210> 110
 <211> 3410
 <212> DNA
 <213> Homo sapien

<400> 110
 gggaaccagc ctgcacgcgc tggctccggg tgacagccgc ggcctcggc caggatctga 60
 gtgatgagac gtgtccccac tgaggtgccc cacagcagca ggtgttgagc atgggctgag 120

aagctggacc	ggcaccaaaag	ggctggcaga	aatggggcgcc	tggctgattc	ctaggcagtt	180
ggcggcagca	aggaggagag	gccgcagctt	ctggagcaga	gccgagacga	agcagttctg	240
gagtgcctga	acggccccct	gagccctacc	cgcttggccc	actatgggtc	agaggctgtg	300
ggtagccgc	ctgctgcggc	accggaagc	ccagctcttg	ctggccaacc	tgctaaccct	360
tggcctggag	gtgtgttttg	ccgcaggcat	cacctatgtg	ccgcctctgc	tgtgtgaagt	420
gggggtagag	gagaagttca	tgaccatggt	gctgggcatt	ggtccagtgc	tgggcctggt	480
ctgtgtcccg	ctcctaggct	cagccagtga	ccactggcgt	ggacgctatg	gccgccgccc	540
gcccttcac	tgggcactgt	ccttgggcat	cctgctgagc	ctctttctca	ccccaaagggc	600
cggctggcta	gcagggtctg	tgtgtcccga	tcccaggccc	ctggagctgg	cactgctcat	660
cctgggcgtg	gggctgctgg	acttctgtgg	ccagggtgtg	ttcactccac	tggaggccct	720
gctctctgac	ctcttccggg	acccggacca	ctgtcgccag	gcctactctg	tctatgcctt	780
catgatcagt	cttgggggct	gcctgggcta	cctcctgcct	gccattgact	gggacaccag	840
tgccctggcc	ccctacctgg	gcacccagga	ggagtgcctc	tttggcctgc	tcacctcat	900
cttccctacc	tgcgtagcag	ccacactgct	ggtgctgag	gaggcagcgc	tgggccccac	960
cgagccagca	gaagggtgtg	cggccccctc	cttgcgccc	cactgctgtc	catgccggggc	1020
ccgcttggct	ttccggaacc	tgggcgcct	gcttccccgg	ctgcaccagc	tgtgtgtccg	1080
catgccccgc	accctgcgcc	ggctcttcgt	ggctgagctg	tgcagctgga	tggcactcat	1140
gaccttcacg	ctgttttaca	cggatttcgt	gggcgagggg	ctgtaccagg	gcgtgccag	1200
agctgagccg	ggcaccgagg	cccggagaca	ctatgatgaa	ggcgttcgga	tgggcagcct	1260
ggggctgttc	ctgcagtgcg	ccatctccct	ggtcttctct	ctggctatgg	accggctggt	1320
gcagcgattc	ggcactcgag	cagtctatct	ggccagtgtg	gcagctttcc	ctgtggctgc	1380
cggtagccaca	tgcctgtccc	acagtgtggc	cgtggtgaca	gcttcagccg	ccctcacggg	1440
gttcaccttc	tcagccctgc	agatcctgcc	ctacacactg	gcctccctct	accaccggga	1500
gaagcaggtg	ttcctgcccc	aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	1560
cctgatgacc	agcttccctg	caggccctaa	gcctggagct	cccttcccta	atggacacgt	1620
gggtgctgga	ggcagtggcc	tgtcccacc	tccaccgcg	ctctgccccg	cctctgctctg	1680
tgatgtctcc	gtacgtgtgg	tgggtgggtga	gcccaccgag	gccagggtgg	ttccggggccg	1740
gggcatctgc	ctggacctcg	ccatcctgga	tagtgccctc	ctgctgtccc	aggtggcccc	1800
atccctgttt	atgggctcca	ttgtccagct	cagccagtct	gtcactgcct	atatgggtgtc	1860
tgccgcagge	ctgggtctgg	tcgccattta	ctttgtctaca	caggtagtat	ttgacaagag	1920
cgacttggcc	aaatactcag	cgtagaaaac	tccagcaca	ttgggtgga	gggctgcct	1980
cactgggtcc	cagctccccg	ctcctgttag	ccccatgggg	ctgccgggct	ggccgccagt	2040
ttctgttgct	gccaaagtaa	tgtggctctc	tgtgtccacc	ctgtgctgct	gagggtgcgta	2100
gctgcacagc	tgggggctgg	ggcgtccctc	tcctctctcc	ccagtctcta	gggctgcctg	2160
actggaggcc	ttccaagggg	gtttcagctc	ggacttatac	agggaggcca	gaagggtccc	2220
atgcactgga	atgcggggac	tctgcagggt	gattacccag	gctcagggtt	aacagctagc	2280
ctcctagtgt	agacacacct	agagaagggt	ttttgggagc	tgaataaaact	cagtccactg	2340
gtttcccatc	tctaagcccc	ttaacctgca	gcttcgttta	atgtagctct	tgcatgggag	2400
ttcttaggat	gaaacactcc	tccatgggat	ttgaacatat	gacttatttg	taggggaaga	2460
gtcctgaggg	gaaacacaca	agaaccaggt	cccctcagcc	cacagcactg	tctttttgct	2520
gatccacccc	cctcttacct	tttatcagga	tgtggcctgt	tggtccttct	gttgccatca	2580
cagagacaca	ggcattttaa	tatttaactt	atttatttaa	caaagtagaa	gggaatccat	2640
tgctagcttt	tctgtgttgg	tgtctaatat	ttgggtaggg	tgggggatcc	ccaacaatca	2700
gggtcccctga	gatagctggt	cattgggctg	atcattgcca	gaatcttctt	ctcctgggggt	2760
ctggccccc	aaaatgccta	accaggacc	ttggaaatc	tactcatccc	aaatgataat	2820
tccaaatgct	gttaccacaag	gttaggggtg	tgaagggaag	tagagggtgg	ggcttcaggt	2880
ctcaaccggt	tccctaacca	ccctcttct	cttggcccag	cctggttccc	cccacttcca	2940
ctccccctca	ctctctctag	gactgggctg	atgaaggcac	tgcccaaaat	ttcccctacc	3000
cccaactttc	ccctaccccc	aactttcccc	accagctcca	caacctgtt	tggagctact	3060
gcaggaccag	aagcacaaaag	tgcggtttcc	caagcctttg	tccatctcag	ccccagagt	3120
atatctgtgc	ttgggggaatc	tcacacagaa	actcaggagc	acccccctgc	tgagctaagg	3180
gaggctctat	ctctcagggg	gggtttaagt	gccgtttgca	ataatgtcgt	cttattttatt	3240
tagcgggggtg	aatattttat	actgtaagt	agcaatcaga	gtataatgtt	tatggtgaca	3300
aaattaaagg	ctttcttata	tgtttaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	3360
aaaaaaaaara	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		3410

<210> 111

<211> 1289

<212> DNA

<213> Homo sapien

<400> 111

```

agccaggcgt cccctctgcct gccactcag tggcaacacc cgggagctgt tttgtccttt 60
gtggagcctc agcagttccc tctttcagaa ctactgccca agagccctga acaggagcca 120
ccatgcagtg cttcagcttc attaagacca tgatgatcct cttcaatttg ctcacttttc 180
tgtgtggtgc agccctgttg gcagtgggca tctgggtgtc aatcgatggg gcatcctttc 240
tgaagatctt cgggccactg tcgtccagtg ccatgcagtt tgtcaacgtg ggctacttcc 300
tcategcagc cggcgtttgt gtctttgtct ttgggttctt gggctgctat ggtgctaaga 360
ctgagagcaa gtgtgccctc gtgacgttct tcttcactct cctcctcatc ttcattgtgt 420
aggttgacgc tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt 480
tgctggtagt gcctgccatc aagaaagatt atggttccca ggaagacttc actcaagtgt 540
ggaacaccac catgaaaggg ctcaagtgtc gtggcttcac caactatacg gattttgagg 600
actcacccta cttcaaagag aacagtgcct ttccccatt ctgttgcaat gacaacgtca 660
ccaacacagc caatgaaacc tgcaccaagc aaaaggctca cgaccaaaaa gtagagggtt 720
gcttcaatca gcttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag 780
ctggaattgg gggcctcgag ctggctgcca tgattgtgtc catgtatctg tactgcaatc 840
tacaataagt ccacttctgc ctctgccact actgctgcca catgggaact gtgaagaggc 900
accctggcaa gcagcagtg ttgggggagg ggacaggatc taacaatgtc acttggggcca 960
gaatggacct gccctttctg ctccagactt ggggctagat agggaccact ccttttagcg 1020
atgcctgact ttccttccat tgggtgggtgg atgggtgggg ggcattccag agcctctaag 1080
gtagccagtt ctgttgccca ttccccagct ctattaaacc cttgatatgc cccctaggcc 1140
tagtggatgat cccagtgtc tactggggga tgagagaaag gcattttata gcctgggcat 1200
aagtgaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc 1260
tgttacaatg ttaaaaaaaaa aaaaaaaaaa 1289

```

<210> 112

<211> 315

<212> PRT

<213> Homo sapien

<400> 112

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1          5          10          15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20          25          30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35          40          45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50          55          60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65          70          75          80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85          90          95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100          105          110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
115          120          125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130          135          140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145          150          155          160
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165          170          175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
180          185          190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu

```

195	200	205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr		
210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		
	245	250
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		
	260	265
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		
	275	280
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly		
290	295	300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		
305	310	315

<210> 113
 <211> 553
 <212> PRT
 <213> Homo sapien

<400> 113		
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala		
1 5 10 15		
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu		
20 25 30		
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val		
35 40 45		
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly		
50 55 60		
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly		
65 70 75 80		
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile		
85 90 95		
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu		
100 105 110		
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly		
115 120 125		
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu		
130 135 140		
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala		
145 150 155 160		
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr		
165 170 175		
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu		
180 185 190		
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu		
195 200 205		
Thr Cys Val Ala Ala Thr Leu Val Ala Glu Glu Ala Ala Leu Gly		
210 215 220		
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His		
225 230 235 240		
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu		
	245	250
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg		
	260	265
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe		
	275	280
		285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

<210> 114

<211> 241

<212> PRT

<213> Homo sapien

<400> 114

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1 5 10 15
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 50 55 60
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 65 70 75 80
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
 85 90 95
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
 100 105 110
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
 115 120 125
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met

130	Lys Gly Leu Lys Cys Cys	135	Gly Phe Thr Asn Tyr	140	Thr Asp Phe Glu Asp
145	Ser Pro Tyr Phe Lys Glu	150	Asn Ser Ala Phe Pro	155	Pro Phe Cys Cys Asn
	165	170		175	
Asp Asn Val Thr Asn Thr	Ala Asn Glu Thr Cys	Thr Lys Gln Lys Ala			
180	185	190			
His Asp Gln Lys Val Glu Gly	Cys Phe Asn Gln Leu Leu Tyr Asp Ile				
195	200	205			
Arg Thr Asn Ala Val Thr Val	Gly Gly Val Ala Ala Gly Ile Gly Gly				
210	215	220			
Leu Glu Leu Ala Ala Met Ile	Val Ser Met Tyr Leu Tyr Cys Asn Leu				
225	230	235		240	
Gln					

<210> 115
 <211> 366
 <212> DNA
 <213> Homo sapien

<400> 115	
gctctttctc tcccctcctc tgaatttaat tctttcaact tgcaatttgc aaggattaca	60
catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac	120
ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga	180
actggtagaa aaacatctga agagctagtc tatcagcatc tgacaggtga attggatggt	240
tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttggtg	300
tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt	360
ttagtc	366

<210> 116
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(282)
 <223> n = A,T,C or G

<400> 116	
acaaagatga accatttcct atattatagc aaaattaaaa tctaccgta ttctaattatt	60
gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa	120
agactttact attttcatat tttaagacac atgatttate ctatttttagt aacctgggtc	180
atacggtaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt	240
tcaatctnga actatctana tcacagacat ttctattcct tt	282

<210> 117
 <211> 305
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(305)
 <223> n = A,T,C or G

<400> 117

```

acacatgtcg cttcactgcc ttcttagatg cttctggta acatanaagga acagggacca 60
tatttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120
aataaggcaa aatatatgaa acaacagggtc tcgagatatt ggaaatcagt caatgaagga 180
tactgatccc tgatcactgt cctaatagcag gatgtgggaa acagatgagg tcacctctgt 240
gactgcccc gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300
tgggt 305

```

```

<210> 118
<211> 71
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(71)
<223> n = A,T,C or G

```

```

<400> 118
accaaggtgt ntgaatctct gacgtgggga tctctgattc cgcacaatc tgagtggaaa 60
aantcctggg t 71

```

```

<210> 119
<211> 212
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(212)
<223> n = A,T,C or G

```

```

<400> 119
actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaagaccaca 60
gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120
agtaagctgg cccttctaataaaaagaaaat tgaaaggttt ctactaanc ggaattaant 180
aatggantca aganactccc aggcctcagc gt 212

```

```

<210> 120
<211> 90
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(90)
<223> n = A,T,C or G

```

```

<400> 120
actcgttgca natcaggggc ccccagagt caccgttgca ggagtccttc tggctttgcc 60
ctccgccggc gcagaacatg ctgggggtgt 90

```

```

<210> 121
<211> 218
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

```


<222> (1)... (218)

<223> n = A,T,C or G

<400> 121

tgtancgtga	anacgacaga	naggggtgtc	aaaaatggag	aanccttgaa	gtcattttga	60
gaataagatt	tgctaaaaga	tttggggcta	aaacatgggt	attgggagac	atttctgaag	120
atatncangt	aaattangga	atgaattcat	ggttcttttg	ggaattcctt	tacgatngcc	180
agcatanact	tcatgtgggg	atancagcta	cccttgta			218

<210> 122

<211> 171

<212> DNA

<213> Homo sapien

<400> 122

taggggtgta	tgcaactgta	aggacaaaaa	ttgagactca	actggcttaa	ccaataaagg	60
catttgtag	ctcatggaac	aggaagtcgg	atgggtggggc	atcttcagtg	ctgcatgagt	120
caccaccccg	gcggggtcat	ctgtgccaca	ggccctgtt	gacagtgcgg	t	171

<210> 123

<211> 76

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (76)

<223> n = A,T,C or G

<400> 123

tgtagcgtga	agacnacaga	atgggtgtgtg	ctgtgetatc	caggaacaca	tttattatca	60
ttatcaanta	ttgtgt					76

<210> 124

<211> 131

<212> DNA

<213> Homo sapien

<400> 124

acctttcccc	aaggccaatg	tectgtgtgc	taactggccg	gctgcaggac	agctgcaatt	60
caatgtgctg	ggcatatgg	aggggaggag	actctaaaat	agccaatttt	attctcttgg	120
ttaagatttg	t					131

<210> 125

<211> 432

<212> DNA

<213> Homo sapien

<400> 125

actttatcta	ctggctatga	aatagatgg	ggaaaattgc	gttaccaact	ataccactgg	60
cttgaaaaag	aggtgatagc	tcttcagagg	acttgtgact	tttgctcaga	tgctgaagaa	120
ctacagtctg	catttggcag	aatgaagat	gaatttggat	taaatgagga	tgctgaagat	180
ttgcctcacc	aaacaaaagt	gaaacaactg	agagaaaatt	ttcaggaaaa	aagacagtgg	240
ctcttgaagt	atcagtcact	tttgagaatg	tttcttagtt	actgcatact	tcatggatcc	300
catgggtggg	gtcttgcate	tgtaagaatg	gaattgattt	tgcttttgca	agaatctcag	360
caggaaacat	cagaaccact	attttctagc	cctctgtcag	agcaaacctc	agtgcctctc	420
ctctttgctt	gt					432

<210> 126
 <211> 112
 <212> DNA
 <213> Homo sapien

<400> 126
 acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60
 agtaagaatg atatttcccc ccagggatca ccaaattttt ataaaaattt gt 112

<210> 127
 <211> 54
 <212> DNA
 <213> Homo sapien

<400> 127
 accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128
 <211> 323
 <212> DNA
 <213> Homo sapien

<400> 128
 acctcattag taattgtttt gttgttttcat ttttttctaa tgtctcccct ctaccagctc 60
 acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca 120
 ttctctctga agtctaggtt acccattttg gggaccatt ataggcaata aacacagttc 180
 ccaaagcatt tggacagttt cttgtttgtg tttagaatgg ttttcctttt tcttagcctt 240
 ttctgcaaa aggctcactc agtcccttgc ttgtcagtg gactgggctc ccaggggcct 300
 aggtgcctt cttttccatg tcc 323

<210> 129
 <211> 192
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(192)
 <223> n = A,T,C or G

<400> 129
 acatacatgt gtgtatatatt ttaaatatca cttttgtatc actctgactt tttagcatac 60
 tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc 120
 tagcacattc atctgtgata naaagatagg tgagtttcat ttcccttcacg ttggccaatg 180
 gataaacaaa gt 192

<210> 130
 <211> 362
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(362)
 <223> n = A,T,C or G

<400> 130
 ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60

```

tataatgacg caacaaaaag gtgctgttta gtcctatggg tcagtttatg cccctgacaa      120
gtttccattg tgttttgccg atcttctggc taatcgtggg atcctccatg ttattagtaa      180
ttctgtattc cattttgtta acgcctggta gatgtaacct gctangaggc taactttata      240
cttatttaaa agctcttatt ttgtgggcat taaaatggca atttatgtgc agcactttat      300
tgcagcagga agcacgtgtg ggttggttgt aaagctcttt gctaattctta aaaagtaatg      360
gg                                                                                   362

```

```

<210> 131
<211> 332
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (332)
<223> n = A,T,C or G

```

```

<400> 131
ctttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca      60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaatgaga      120
gttctccag gtccgcttg ctgctccaag tctcagcagc agcctctttt aggaggcatc      180
ttctgaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa      240
cttccatctg ttatcactgg agaaagccca gactccccaan gacnggtacg gattgtgggc      300
atanaaggat tgggtgaagc tggcgttgtg gt                                                                                   332

```

```

<210> 132
<211> 322
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (322)
<223> n = A,T,C or G

```

```

<400> 132
acttttgcca ttttgtatat ataaacaatc ttgggacatt ctctgaaaa ctagggtgtcc      60
agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat      120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggaccttg tatctcgggt      180
tttagcaagt taaaatgaan atgacaggaa aggcttattt atcaacaaag agaagagttg      240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct      300
gtaacaatct acaattgggc ca                                                                                   322

```

```

<210> 133
<211> 278
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (278)
<223> n = A,T,C or G

```

```

<400> 133
acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt      60
cttggttttc tttccatctg gctcctgggt tgacaatttg tggaacaac tctattgcta      120
ctattttaaa aaaatcacia atctttccct ttaagctatg ttnaattcaa actattcctg      180
ctattcctgt ttgtcaaaag aaattatatt ttcaaaaata tgtntatttg ttgatgggt      240

```

cccacgaaac actaataaaa accacagaga ccagcctg

278

<210> 134
 <211> 121
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(121)
 <223> n = A,T,C or G

<400> 134
 gtttanaaaa cttgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca 60
 tgattctctg aggttaaact tggttttcaa atgttatatt tacttgtatt ttgcttttgg 120
 t 121

<210> 135
 <211> 350
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(350)
 <223> n = A,T,C or G

<400> 135
 acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctataacc 60
 atancaagtg gtgactgggt aagcgtgcga caaagggtcag ctggcacatt acttgtgtgc 120
 aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggactcca 180
 ggggtgcccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgtc 240
 ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag 300
 tteccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt 350

<210> 136
 <211> 399
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(399)
 <223> n = A,T,C or G

<400> 136
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60
 gctgtgattg tatccgaata ntccctcgta gaaaagataa tgagatgacg tgagcagcct 120
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180
 cctggcggcc agccagccag ccacaggtgg gcttcttctt tttgtggtga caacnccaag 240
 aaaactgcag agggccaggg tcaggtgtna gtgggtangt gaccataaaa caccaggtgc 300
 tcccaggaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137
 <211> 165
 <212> DNA
 <213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(165)
<223> n = A,T,C or G

<400> 137
actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60
ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120
ttggtgtggt ccactggtgg tcactgtcat tgggtggggt cctgt 165

<210> 138
<211> 338
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(338)
<223> n = A,T,C or G

<400> 138
actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60
ttaacttctc cagttaagaat cagggacttg aaatggaaac gttaacagcc acatgcccaa 120
tgctgggcag tctcccatgc cttccacagt gaaagggctt gagaaaaatc acatccaatg 180
tcatgtgttt ccagccacac caaaagggtgc ttgggggtgga gggctggggg catananggt 240
cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa 300
aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139
<211> 382
<212> DNA
<213> Homo sapien

<400> 139
gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa 60
gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccgaa gtgaaggaga 120
attcaaacag acctcgatc tcttggtgtg agcctggctg gctcacgcc tatcatctgc 180
atttgctta ctcaggtgct accggactct ggcccctgat gtctgtagtt tcacaggatg 240
ccttatttgt cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat 300
gtcagctatg tgccccatcc tccttcacgc cctccctccc tttcctacca ctgctgagtg 360
gcctggaact tgtttaaggt gt 382

<210> 140
<211> 200
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(200)
<223> n = A,T,C or G

<400> 140
accaaaactt ctttctgttg tgttngattt tactataggg gtttngcttn ttctaaanat 60
acttttcatt taacancttt tgttaagtgt caggctgcac tttgctccat anaattattg 120
ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt 180
atattcagca taaaggagaa 200

<210> 141
 <211> 335
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(335)
 <223> n = A,T,C or G

<400> 141
 actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggtgg 60
 ggggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc aggggtttgtt 120
 atgcatgtag agaaccctaaa ctaattttatt aaacaggata gaaacaggct gtctgggtga 180
 aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg 240
 tttttctacc agttcagaga tnggttaatg actanttcca atgggggaaaa agcaagatgg 300
 attcacaac caagtaattt taaacaaaga cactt 335

<210> 142
 <211> 459
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(459)
 <223> n = A,T,C or G

<400> 142
 accagggttaa tattgccaca tatatccttt ccaattgctg getaaacaga cgtgtattta 60
 ggggtgttta aagacaaccc agcttaatat caagagaaat tgtgaccttt catggagtat 120
 ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca 180
 cacatggctc aacaacactc aaataataaa tcaaataatna tcagatgtta aagattggtc 240
 ttcaaacatc atagccaatg atgccccgct tgcctataat ctctccgaca taaaaccaca 300
 tcaacacctc agtggccacc aaaccattca gcacagcttc cttaactgtg agctgtttga 360
 agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct 420
 cagcanggtt gggaggaacc agtcaacct tggcgtant 459

<210> 143
 <211> 140
 <212> DNA
 <213> Homo sapien

<400> 143
 acatttctct ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg 60
 aaatccaaac agtctctcct agaaaggaat agtgtcacca accccaccca tctccctgag 120
 accatccgac ttcctgtgt 140

<210> 144
 <211> 164
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(164)
 <223> n = A,T,C or G

<400> 144
 acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60
 atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta tacaaaattg 120
 aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt 164

<210> 145
 <211> 303
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(303)
 <223> n = A,T,C or G

<400> 145
 acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa 60
 actggagggt atttataccc aattatccca ttcattaaca tgccctcttc ctccaggctat 120
 gcaggacagc tatcataagt cggcccaggc atccagatac taccatttgc ataaacttca 180
 gtaggggagt ccatccaagt gacagggtcta atcaaaggag gaaatggaac ataagccag 240
 tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgccgtgg tgattaccat 300
 caa 303

<210> 146
 <211> 327
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 146
 actgcagctc aattagaagt ggtctctgac tttcatcanc ttctccctgg gctccatgac 60
 actggcctgg agtgactcat tgctctgggt ggttgagaga gctcctttgc caacaggcct 120
 ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180
 cctgaacagg gaggggtgga ggagccagca tggaacaagc tgccactttc taaagtagcc 240
 agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300
 taggggtgag ctgtgtgact ctatgggt 327

<210> 147
 <211> 173
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(173)
 <223> n = A,T,C or G

<400> 147
 acattgtttt tttagataa agcattgana gagctctcct taacgtgaca caatggaagg 60
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgcctg 120
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148

<211> 477
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(477)
<223> n = A,T,C or G

<400> 148
acaaccactt tatctcatcg aattttttaac ccaaactcac tcactgtgcc tttctatcct 60
atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120
gccctactac ctgctgcaat aatcacattc ccttctgtgc ctgaccctga agccattggg 180
gtggtcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgctcac 240
nccancccac ctcaccgacc ccatectctt acacagctac ctccttgctc tctaacccca 300
tagattatnt ccaaattcag tcaattaagt tactattaac actctaccg acatgtccag 360
caccactggg aagccttctc cagccaacac acacacacac acacncacac acacacatat 420
ccaggcacag gctacctcat cttcacaatc acccctttaa ttaccatgct atggtgg 477

<210> 149
<211> 207
<212> DNA
<213> Homo sapien

<400> 149
acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac 60
taacgtatatt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct 120
gatgataaat aagagtcagc caggtaagtg ggtgggtgtg tatgggcaca gtgaagaaca 180
tttcaggcag agggaacagc agtgaaga 207

<210> 150
<211> 111
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(111)
<223> n = A,T,C or G

<400> 150
accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg 60
cacttaaagt tggtcagtgt ttggacttgt taactantgg catctttggg t 111

<210> 151
<211> 196
<212> DNA
<213> Homo sapien

<400> 151
agcgcggcag gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac 60
agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat 120
ggataccaac cggaaaaccc ctatcccgcg cagccactg tgggtccccc tgtctacgag 180
gtgcatccgg ctcagt 196

<210> 152
<211> 132
<212> DNA

<213> Homo sapien

<400> 152

acagcacttt cacatgtaag aagggagaaa ttcctaaatg taggagaaag ataacagAAC	60
cttccccctt tcatctagtG gtggaaacct gatgctttat gttgacagga atagaaccag	120
gagggagttt gt	132

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(285)

<223> n = A,T,C or G

<400> 153

acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag	60
cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctcagcagga	120
gcacatcaat aaagtccaaa gtcttggaact tggccttggc ttggaggaag tcatcaacac	180
cctggctagt gaggggtgagg cgccgctcct ggatgacggc atctgtgaag tcgtgcacca	240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt	285

<210> 154

<211> 333

<212> DNA

<213> Homo sapien

<400> 154

accacagtcc tgttgggcca gggcttcatg accctttctg tgaaaagcca tattatcacc	60
accccaaatt tttccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac	120
cctaagccgg ttacacagct aactcccact ggccctgatt tgtgaaattg ctgctgcctg	180
attggcacag gagtcgaagg tgttcagctc cctctctcgg tggaaagaga ctctgatttg	240
agtttcacaa attctcgggc cacctcgtca ttgctcctct gaaataaaat ccggagaatg	300
gtcaggcctg tctcatccat atggatcttc cgg	333

<210> 155

<211> 308

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(308)

<223> n = A,T,C or G

<400> 155

actggaaata ataaaaccca catcacagtG ttgtgtcaaa gatcatcagg gcatggatgg	60
gaaagtgttt tgggaactgt aaagtgccta acacatgatc gatgattttt gttataatat	120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcccc	180
atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggct	240
gcttttagcc tccanaagtt tctctgaagc caaccaaac tctangtgta aggcagtctg	300
gccctggg	308

<210> 156

<211> 295

<212> DNA

<213> Homo sapien

<400> 156

accttgctcg	gtgcttgga	catattagga	actcaaaata	tgagatgata	acagtgccta	60
ttattgatta	ctgagagaac	tgtagacat	ttagttgaag	atcttctaca	caggaactga	120
gaataggaga	ttatgttttg	cctcatatt	ctctcctatc	ctccttgcoct	cattctatgt	180
ctaataatatt	ctcaatcaaa	taagggttagc	ataatcagga	aatcgaccaa	ataccaatat	240
aaaaccagat	gtctatcctt	aagattttca	aatagaaaac	aaattaacag	actat	295

<210> 157

<211> 126

<212> DNA

<213> Homo sapien

<400> 157

acaagtttaa	atagtgtgt	cactgtgcat	gtgctgaaat	gtgaaatcca	ccacatttct	60
gaagagcaaa	acaaattctg	tcatgtaac	tctatcttgg	gtcgtgggta	tatctgtccc	120
cttagt						126

<210> 158

<211> 442

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(442)

<223> n = A,T,C or G

<400> 158

acccactggt	cttggaaca	cccatcctta	atacgatgat	ttttctgtcg	tgtgaaaatg	60
aanccagcag	gctgccccta	gtcagtcctt	ccttccagag	aaaaagagat	ttgagaaagt	120
gcctgggtaa	ttcaccatta	atttcctccc	ccaaactctc	tgagtcttcc	cttaatatatt	180
ctggtgggtc	tgaccaaagc	aggtcatggt	ttggtgagca	tttgggatcc	cagtgaagta	240
natgtttgta	gccttgcata	cttagccctt	cccacgcaca	aacggagtgg	cagagtgggtg	300
ccaaccctgt	tttcccagtc	cacgtagaca	gattcacagt	gcggaattct	ggaagctgga	360
nacagacggg	ctctttgcag	agccgggact	ctgagangga	catgagggcc	tctgcctctg	420
tgttcattct	ctgatgtcct	gt				442

<210> 159

<211> 498

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(498)

<223> n = A,T,C or G

<400> 159

acttccaggt	aacgttggtg	tttccgttga	gcctgaactg	atgggtgacg	ttgtagggtc	60
tccaacaaga	actgagggtg	cagagcgggt	aggggaagagt	gctgttccag	ttgcacctgg	120
gctgctgtgg	actggttggtg	attcctcact	acggcccaag	gttgtggaac	tggcanaaag	180
gtgtgttggt	gganttgagc	tcgggcggct	gtggttaggt	gtgggtctct	caacaggggc	240
tgctgtgggtg	ccgggangtg	aangtggtgt	gtcacttgag	cttggccagc	tctggaaagt	300
antanattct	tcctgaaggc	cagcgcttgt	ggagctggca	ngggtcantg	ttgtgtgtaa	360
cgaaccagtg	ctgctgtggg	tgggtgtana	tcctccacaa	agcctgaagt	tatggtgtcn	420
tcaggaana	atgtgggttc	agtgtccctg	ggcngctgtg	gaaggttgta	nattgtcacc	480

aaggggaataa gctgtggt

498

<210> 160
<211> 380
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

<400> 160

acctgcatcc	agcttcctcg	ccaaactcac	aaggagacat	caacctctag	acagggaaac	60
agcttcagga	tacttccagg	agacagagcc	accagcagca	aaacaaatat	tcccâtgcct	120
ggagcatggc	atagaggaag	ctganaaatg	tggggtctga	ggaagccatt	tgagtctggc	180
cactagacat	ctcatcagcc	acttgtgtga	agagatgccc	catgaccca	gatgcctctc	240
ccacccttac	ctccatctca	cacacttgag	ctttccactc	tgtataattc	taacatcctg	300
gagaaaaatg	gcagtttgac	cgaacctgtt	cacaacggta	gaggctgatt	tctaacgaaa	360
cttgtagaat	gaagcctgga					380

<210> 161
<211> 114
<212> DNA
<213> Homo sapien

<400> 161

actccacatc	ccctctgagc	aggcggttgt	cgttcaaggt	gtatttggcc	ttgcctgtca	60
cactgtccac	tggcccctta	tccacttggt	gcttaatccc	tcgaaagagc	atgt	114

<210> 162
<211> 177
<212> DNA
<213> Homo sapien

<400> 162

actttctgaa	tcgaatcaaa	tgatacttag	tgtagtttta	atatacctcat	atatatcaaa	60
gttttactac	tctgataatt	ttgtaaacca	ggtaaccaga	acatccagtc	atacagcttt	120
tgggtgatata	taacttggca	ataaccagtc	ctggtgatac	ataaaaactac	tcactgt	177

<210> 163
<211> 137
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(137)
<223> n = A,T,C or G

<400> 163

catttatata	gacaggcgtg	aagacattca	cgacaaaaac	gcgaaattct	atcccgtgac	60
canagaaggc	agctacggct	actcctacat	cctggcgtgg	gtggccttcg	cctgcacctt	120
catcagcggc	atgatgt					137

<210> 164
<211> 469
<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(469)

<223> n = A,T,C or G

<400> 164

cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta	60
tgcaatgcat catgctatct catacctaata gagggagttc caggagattc aaccaggaaa	120
tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt	180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg	240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg	300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct	360
tctagtaggc acagggctcc caggccaggc ctcatctctc tctggcctct aatagtcaat	420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt	469

<210> 165

<211> 195

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(195)

<223> n = A,T,C or G

<400> 165

acagtttttt atanatatcg acattgccgg cacttgtgtt cagtttcata aagctgggtg	60
atccgctgtc atccactatt ccttggttag agtaaaaatt attcttatag cccatgtccc	120
tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact	180
tcctctgaga tgagt	195

<210> 166

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 166

acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc	60
cgagggtcga gtccacacca ccggtgtagg tgtgctcaat cttgggcttg gcgcccacct	120
ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt	180
tttgagacc agcctgagca aggggcggat gttagcttc agtcctcct tcgtcagggtg	240
gatgccaaacc tcgtctangg tccgtgggaa gctgggtgtc acntcaccta caacctgggc	300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt	360
nggggccttt ttggtgaact ttc	383

<210> 167

<211> 247

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(247)
 <223> n = A,T,C or G

<400> 167

acagagccag	accttggcca	taaataaanc	agagattaag	actaaacccc	aagtcganat	60
tggagcagaa	actggagcaa	gaagtgggcc	tggggctgaa	gtagagacca	aggccactgc	120
tatanccata	cacagagcca	actctcaggc	caaggcnatg	gttggggcag	anccagagac	180
tcaatctgan	tcctaaagtgg	tggctggaac	actggtcatg	acanaggcag	tgactctgac	240
tgangtc						247

<210> 168
 <211> 273
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(273)
 <223> n = A,T,C or G

<400> 168

acttctaagt	tttctagaag	tggaaggatt	gtantcatcc	tgaaaatggg	tttacttcaa	60
aatccctcan	ccttgttctt	cacnactgtc	tatactgana	gtgtcatggt	tccacaaagg	120
gctgacacct	gagcctgnat	tttactcat	ccctgagaag	ccctttccag	taggggtggc	180
aattcccaac	ttccttgcca	caagcttccc	aggctttctc	ccctggaaaa	ctccagcttg	240
agtcaccgat	acactcatgg	gctgccctgg	gca			273

<210> 169
 <211> 431
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(431)
 <223> n = A,T,C or G

<400> 169

acagccttgg	cttccccaaa	ctccacagtc	tcagtgcaga	aagatcatct	tccagcagtc	60
agctcagacc	agggtcaaaag	gatgtgacat	caacagtttc	tggtttcaga	acagggttcta	120
ctactgtcaa	atgaccccc	atacttcctc	aaaggctgtg	gtaagttttg	cacagggtgag	180
ggcagcagaa	agggggtant	tactgatgga	caccatcttc	tctgtatact	ccacactgac	240
cttgccatgg	gcaaaggccc	ctaccacaaa	aacaatagga	tcactgctgg	gcaccagctc	300
acgcacatca	ctgacaaccg	ggatggaaaa	agaantgcc	actttcatac	atccaactgg	360
aaagtgatct	gatactggat	tcttaattac	cttcaaaaagc	ttctgggggc	catcagctgc	420
tcgaacactg	a					431

<210> 170
 <211> 266
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(266)
 <223> n = A,T,C or G

<400> 170
 acctgtgggc tgggctgtta tgcctgtgcc ggctgctgaa agggagttca gaggtggagc 60
 tcaaggagct ctgcaggcat tttgccaanc ctctccanag canaggggagc aacctacact 120
 ccccgctaga aagacaccag attggagtc tgggaggggg agttgggggtg ggcatttgat 180
 gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240
 tcaaagctag gggctctggca ggtgga 266

<210> 171
 <211> 1248
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (1248)
 <223> n = A,T,C or G

<400> 171
 ggcagccaaa tcataaacgg cgaggactgc agcccgact cgcagccctg gcaggcggca 60
 ctggtcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcacccgca gtgggtgctg 120
 tcagccgcac actgtttcca gaagtgaagt cagagctcct acaccatcgg gctgggcctg 180
 cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta 240
 cggcaccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac 300
 gaatccgtgt ccgagctcga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360
 gcggggaaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420
 gtgctgcagt gcgtgaacgt gtcggtggtg tctgaggagg tctgcagtaa gctctatgac 480
 ccgctgtacc accccagcat gttctgcgcc ggcggaggggc aagaccagaa ggactcctgc 540
 aacggtgact ctgggggggccc cctgatctgc aacgggtact tgcagggcct tgtgtcttcc 600
 ggaaaagccc cgtgtggcca agttggcgtg ccaggtgtct acaccaacct ctgcaaattc 660
 actgagtggga tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa 720
 attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agccccctct 780
 ccctcaggcc caggagtcca ggccccccag cctcctctcc tcaaaccaag ggtacagatc 840
 cccagccctc cctccctcag acccaggagt ccagaccccc cagccccctc tccctcagac 900
 ccaggagtcc agccccctcct cctcagacc caggagtcca gacccccag cccctcctcc 960
 ctcagacca ggggtccagg cccccaaccc ctcctcctcc agactcagag gtccaagccc 1020
 ccaaccntc attccccaga cccagaggtc caggteccag cccctcntcc ctcagacca 1080
 gcggtccaat gccacctaga ctntccctgt acacagtgcc cccttgtggc acgttgacct 1140
 aaccttacca gttgggtttt catttttngt ccctttcccc tagatccaga aataaagttt 1200
 aagagaagng caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1248

<210> 172
 <211> 159
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1) ... (159)
 <223> Xaa = Any Amino Acid

<400> 172
 Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 1 5 10 15
 Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20 25 30
 Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 35 40 45
 Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly

50	55	60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu		
65	70	75
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe		80
	85	90
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser		95
	100	105
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe		110
	115	120
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn		125
	130	135
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser		140
145	150	155

<210> 173

<211> 1265

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1265)

<223> n = A,T,C or G

<400> 173

ggcagcccg	actcgcagcc	ctggcaggcg	gcactgggtca	tggaaaacga	attgttctgc	60
tcgggcgtcc	tggtgcatcc	gcagtgggtg	ctgtcagccg	cacactgttt	ccagaactcc	120
tacaccatcg	ggctgggcct	gcacagtctt	gaggccgacc	aagagccagg	gagccagatg	180
gtggaggcca	gcctctccgt	acggcaccca	gagtacaaca	gacccttgct	cgctaacgac	240
ctcatgtcca	tcaagttgga	cgaatccgtg	tccgagtctg	acaccatccg	gagcatcagc	300
attgcttcgc	agtgccctac	cgcggggaac	tcttgectcg	tttctggctg	gggtctgctg	360
gcgaacggtg	agctcacggg	tgtgtgtctg	ccctcttcaa	ggaggctctc	tgccagtcg	420
cgggggctga	cccagagctc	tgcgtcccag	gcagaatgcc	taccgtgctg	cagtgcgtga	480
acgtgtcggt	ggtgtctgag	gaggtctgca	gtaagctcta	tgaccgcgtg	taccacccca	540
gcatgttctg	cgccggcgga	gggcaagacc	agaaggactc	ctgcaacggt	gactctgggg	600
ggccccctgat	ctgcaacggg	tacttgagg	gccttggtgc	tttcggaaaa	gccccgtgtg	660
gccaaagtgg	cgtgccaggt	gtctacacca	acctctgcaa	attcactgag	tggatagaga	720
aaaccgtcca	ggccagttaa	ctctggggac	tgggaaccca	tgaaattgac	ccccaaatac	780
atcctgcgga	aggaattcag	gaatatctgt	tcccagcccc	tcctccctca	ggcccaggag	840
tccaggcccc	cagcccctcc	tccctcaaac	caagggtaca	gatccccagc	ccctectccc	900
tcagacccag	gagtcacag	ccccagccc	ctcctccctc	agaccagga	gtccagcccc	960
tcctcctca	gaccaggag	tccagacccc	ccagccccctc	ctccctcaga	cccaggggtt	1020
gaggccccca	acccctcctc	cttcagagtc	agagggtcaa	gcccccaacc	cctcgttccc	1080
cagaccaga	ggttnaggtc	ccagccccctc	ttcctcaga	cccagnggtc	caatgccacc	1140
tagattttcc	ctgnacacag	tgcccccttg	tggnangttg	acccaacctt	accagttggt	1200
ttttcatttt	tngtcccttt	cccctagatc	cagaaataaa	gtttaagaga	ngngcaaaaa	1260
aaaaa						1265

<210> 174

<211> 1459

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1459)

<223> n = A,T,C or G

<400> 174

ggtcagccgc	acactgtttc	cagaagttag	tgcagagctc	ctacaccatc	gggctggggc	60
tgcacagtct	tgaggccgac	caagagccag	ggagccagat	ggtggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgctaacga	cctcatgctc	atcaagttgg	180
acgaatccgt	gtccgagtct	gacaccatcc	ggagcatcag	cattgcttcg	cagtgcctta	240
ccgcggggaa	ctcttgcttc	gtttctggct	ggggtctgct	ggcgaacggg	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggctct	ctgcccagtc	gcgggggctg	acccagagct	360
ctgcgtccca	ggcagaatgc	ctaccgtgct	gtaccacccc	ancatgttct	gcgcggcgg	420
ngaggctctgc	antaagctct	atgacccgct	gtaccacccc	ancatgttct	gcgcggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcagggcact	540
cagggaaggg	tggagaaggg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
atggagagac	acacagggag	acagtgacaa	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaagga	agagagaaac	agaaacagac	atggggaggg	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcatggggcc	tgagggcggg	780
gacctccacc	caatagaaaa	tcctcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtcgattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttgga	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	ttttttaaat	tggtgcaact	ctcctaataa	ttttctgatg	tggtttattga	1020
aaaaatccaa	gtataagtgg	acttggtgat	tcaaaccagg	gttggttcaag	gggtcaactgt	1080
gtaccagag	ggaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aatcaagac	tctacaaaga	ggctgggcag	ggtgggtcat	gcctgtaatc	ccagcacttt	1200
gggagggcag	gcaggcagat	cacttgaggt	aaggagttca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatgggtgg	aggcgctgt	1320
aatcccagct	acttgggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagaggtt	1380
gaagtgaagt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaa					1459

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1167)

<223> n = A,T,C or G

<400> 175

gcgcagccct	ggcaggcggc	actgggtcatg	gaaaacgaat	tggtctgctc	gggcgtcctg	60
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	120
ctgggctctg	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	180
ctctccgtac	ggcaccacga	gtacaacaga	ctcttgctcg	ctaacgacct	catgctcatc	240
aagttggacg	aatccgtgtc	cgagtctgac	accatccgga	gcacagcat	tgcttcgcag	300
tgccctaccg	cggggaaactc	ttgcctcgtn	tctggctggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcaactg	cgtgaacgtg	tcgggtggtg	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgccg	gcggagggca	agaccagaag	480
gactcctgca	acggtgactc	tggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
gtgtctttcg	gaaaagcccc	gtgtggccaa	cttggcgtgc	caggtgtcta	caccaacctc	600
tgcaaattca	ctgagtggat	agagaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgaccccc	aatacatcct	gcggaangaa	ttcaggaata	tctgttccca	720
gcccctcctc	cctcaggccc	aggagtccag	gccccagcc	cctcctcctt	caaaccaagg	780
gtacagatcc	ccaggccctc	ctccctcaga	cccaggagtc	cagaccccc	agccccctnt	840
ccntcagacc	caggagttcca	gcccctcctc	cntcagacgc	aggagtccag	acccccagc	900
ccntcctcgg	tcagaccag	gggtgcaggc	cccccaaccc	tcntccntca	gagtcagagg	960
tccaagcccc	caacccctcg	ttccccagac	ccagaggtnc	aggtcccagc	ccctcctccc	1020
tcagaccag	cggtccaatg	ccacctagan	tntccctgta	cacagtgcc	ccttgtggca	1080
ngttgacca	accttaccag	ttggtttttc	attttttgtc	cctttccctt	agatccagaa	1140
ataaagtnta	agagaagcgc	aaaaaaa				1167

<210> 176
 <211> 205
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(205)
 <223> Xaa = Any Amino Acid

<400> 176
 Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1 5 10 15
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20 25 30
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35 40 45
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
 50 55 60
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65 70 75 80
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85 90 95
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
 100 105 110
 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
 115 120 125
 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
 130 135 140
 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
 145 150 155 160
 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
 165 170 175
 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
 180 185 190
 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
 195 200 205

<210> 177
 <211> 1119
 <212> DNA
 <213> Homo sapien

<400> 177
 gcgcactcgc agccctggca ggcggcactg gtcattggaaa acgaattggt ctgctcgggc 60
 gtcttggtgc atccgcagt ggtgctgtca gccgcacact gttccagaa ctctacacc 120
 atcgggtgg gctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag 180
 gccagcctct ccgtacggca cccagagtag aacagaccct tgctcgctaa cgacctcatg 240
 ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct 300
 tcgcagtgcc ctaccgcggg gaactcttgc ctctgttctg gctggggtct gctggcgaac 360
 gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420
 caaccctggc aggggtgtac catttcggca acttccagt caaggacgtc ctgctgcac 480
 ctactgggt gctcactact gctcactgca tcaccggaa cactgtgatc aactagccag 540
 caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600
 actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660
 cagttatcct cactgaattg agatttctctg cttcagtgtc agccattccc acataatttc 720
 tgacctacag aggtgaggga tcatatagct cttcaaggat gctgggtact ccctcacaaa 780

```

ttcatttctc ctgtttagt gaaaggtgcg ccctctggag cctcccaggg tgggtgtgca      840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg      900
ctcagtaacac cagggcaggt ctgacatttc ttcatttagt gtatgctgtc cattcatgca      960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg     1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc     1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaaa     1119

```

<210> 178
 <211> 164
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(164)
 <223> Xaa = Any Amino Acid

```

<400> 178
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
          20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
          35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
          50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
          85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
          100          105          110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
          115          120          125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
          130          135          140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145          150          155          160
Pro Gly Thr Leu

```

<210> 179
 <211> 250
 <212> DNA
 <213> Homo sapien

```

<400> 179
ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct      60
ccagctgccc ccggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct     120
gccaggcact gtcatctca gcttttctgt ccctttgttc ccggcaagcg cttctgctga     180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa     240
aaaaaaaaaa                                     250

```

<210> 180
 <211> 202
 <212> DNA
 <213> Homo sapien

<400> 180

actagtccag	tgtggtggaa	ttccattgtg	ttggggccaa	cacaatggct	acctttaaca	60
tcacccagac	cccgccctg	cccgtgccc	acgctgctgc	taacgacagt	atgatgctta	120
ctctgctact	cggaaactat	ttttatgtaa	ttaatgtatg	ctttcttggt	tataaatgcc	180
tgatttaaaa	aaaaaaaaaa	aa				202

<210> 181

<211> 558

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (558)

<223> n = A,T,C or G

<400> 181

tccttttgkt	naggtttkkg	agacamccck	agacctwaan	ctgtgtcaca	gacttcyngg	60
aatgttttagg	cagtgtcagt	aatttcytcg	taatgattct	gttattactt	tcctnattct	120
ttattcctct	ttcttctgaa	gattaatgaa	gttgaaaatt	gaggtggata	aatacaaaaa	180
ggtagtgtga	tagtataagt	atctaagtgc	agatgaaagt	gtgttatata	tatccattca	240
aaattatgca	agttagtaat	tactcagggt	taactaaatt	actttaatat	gctgttgaac	300
ctactctgtt	ccttggtcag	aaaaaattat	aaacaggact	ttggttagtt	gggaagccaa	360
attgataata	ttctatgttc	taaaagttgg	gctatacata	aattattaag	aaatatggaw	420
ttttattccc	aggaatatgg	kgttcatttt	atgaatatta	cscrggatag	awgtwtgagt	480
aaaaycagtt	ttggtwaata	ygtwaatatg	tcmtaaataa	acaakgcttt	gacttatttc	540
caaaaaaaaa	aaaaaaaaa					558

<210> 182

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (479)

<223> n = A,T,C or G

<400> 182

acagggwttk	grggatgcta	agscgccrga	rwtygtttga	tccaaccctg	gcttwttttc	60
agaggggaaa	atggggccta	gaagttacag	mscatytagy	tggtgcgmtg	gcacccctgg	120
cstcacacag	astcccgagt	agctgggact	acaggcacac	agtcactgaa	gcaggccctg	180
ttwgcaattc	acgttgccac	ctccaactta	aacattcttc	atatgtgatg	tccttagtca	240
ctaagggtta	actttcccac	ccagaaaagg	caacttagat	aaaatcttag	agtactttca	300
tactmttcta	agtcctcttc	cagcctcact	kkgagtcctm	cytggggggt	gataggaant	360
ntctcttggc	tttctcaata	aartctctat	ycatctcatg	tttaatttgg	tacgcataa	420
awtgstgara	aaattaaaa	gttctgggty	mactttaaaa	aaaaaaaaaa	aaaaaaaaa	479

<210> 183

<211> 384

<212> DNA

<213> Homo sapien

<400> 183

aggcgggagc	agaagctaaa	gccaaagccc	aagaagagtg	gcagtgccag	cactgggtgcc	60
agtaccagta	ccaataacag	tgccagtgcc	agtgccagca	ccagtgggtg	cttcagtgtc	120
ggtgccagcc	tgaccgccac	tctcacattt	gggtctctcg	ctggccttgg	tgagctgggt	180
gccagcacca	gtggcagctc	tggtgcctgt	ggtttctcct	acaagtgaga	ttttagatat	240

tgттаатсст	gccagtcttt	ctcttcaagc	cagggtgcat	cctcagaaac	ctactcaaca	300
cagcactcta	ggcagccact	atcaatcaat	tgaagttgac	actctgcatt	aratctattt	360
gccatttcaa	aaaaaaaaaa	aaaa				384

<210> 184
 <211> 496
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(496)
 <223> n = A,T,C or G

<400> 184						
accgaattgg	gaccgctggc	ttataagcga	tcatgtyynt	ccrgtatcac	ctcaacgagc	60
agggagatcg	agtcctatacg	ctgaagaaat	ttgacccgat	gggacaacag	acctgctcag	120
cccattctgc	tcggttctcc	ccagatgaca	aatactctsg	acaccgaatc	accatcaaga	180
aacgcttcaa	ggtgctcatg	accagcaac	cgcgccctgt	cctctgaggg	tcctttaaac	240
tgatgtcttt	tctgccacct	gttacccttc	ggagactccg	taaccaaact	cttcggactg	300
tgagccctga	tgcccttttg	ccagccatac	tctttggcat	ccagtctctc	gtggcgattg	360
attatgcttg	tgtgaggcaa	tcatggtggc	atcacccata	aagggaacac	atttgacttt	420
tttttctcat	attttaaatt	actacmagaw	tattwmagaw	waaatgawtt	gaaaaactst	480
taaaaaaaaa	aaaaaa					496

<210> 185
 <211> 384
 <212> DNA
 <213> Homo sapien

<400> 185						
gctggtagcc	tatggcgkgg	cccacggagg	ggctcctgag	gccacggrac	agtgacttcc	60
caagtatcyt	gcgcsgcgtc	ttctaccgtc	cctacctgca	gatcttcggg	cagaattcccc	120
aggaggacat	ggacgtggcc	ctcatggagc	acagcaactg	ytcgctcgag	cccggcttct	180
gggcacaccc	tctgggggcc	caggcgggca	cctgcgtctc	ccagtatgcc	aactggctgg	240
tggtgctgct	cctcgctcatc	ttcctgctcg	tggccaacat	cctgctggtc	aacttgctca	300
ttgccatgtt	cagttacaca	ttcggcaaag	tacagggcaa	cagcgatctc	tactgggaag	360
gcgcagcggt	accgcctcat	ccgg				384

<210> 186
 <211> 577
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(577)
 <223> n = A,T,C or G

<400> 186						
gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cytcctggca	tcttggggcg	gcntaatatt	120
ccaggaaaact	ctcaatcaag	tcaccgtcga	tgaaacctgt	gggctgggtc	tgtcttcgcg	180
tcggtgtgaa	aggatctccc	agaaggagtg	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtaaccag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgccgttga	mcgtgccgaa	garcaccgag	ccttggtgtg	gggkkgaaagt	360
ctcacccaga	ttctgcatta	ccagagagcc	gtggcaaaaag	acattgacaa	actcgcccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcctc	gtcmgttggt	ggcagcgctw	480

tcccttttgac acacaaacaa gttaaaggca ttttcagccc ccagaaantt gtcatcatcc 540
aagatntcgc acagcactna tccagttggg attaaat 577

<210> 187

<211> 534

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(534)

<223> n = A,T,C or G

<400> 187

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctgggtattaa	aattcacaaat	atgcaacact	120
ttaaaccagt	gtgcaatctg	ctcccyynac	tttgtcatca	ccagtctggg	aakaagggtg	180
tgccctattc	acacctgtta	aaagggcgct	aagcattttt	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagtaaac	agttatyaat	ttgttagcca	attcactttc	300
ttcatgggac	agagccatyt	gatttaaaaa	gcaaattgca	taatattgag	cttygggagc	360
tgatatttga	gcggaagagt	agccttttcta	cttcaccaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgttctg	480
aggatctccc	agtttatatta	ccacttgcac	aagaaggcgt	tttcttcctc	agge	534

<210> 188

<211> 761

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(761)

<223> n = A,T,C or G

<400> 188

agaaaccagt	atctctnaaa	acaacctctc	ataccttggtg	gacctaat	ttgtgtgcgtg	60
tgtgtgtgcg	cgcataattat	atagacaggc	acatcttttt	tacttttgta	aaagcttatg	120
cctctttggg	atctatatct	gtgaaagttt	taatgatctg	ccataatgtc	ttggggacct	180
ttgtcttctg	tgtaaatggg	actagagaaa	acacctatnt	tatgagtcaa	tctagttngt	240
tttattcgac	atgaaggaaa	tttccagatn	acaacactna	caaactctcc	ctkgackarg	300
ggggacaaag	aaaagcaaaa	ctgamcataa	raaacaatwa	cctggtgaga	arttgcataa	360
acagaaatwr	ggtagtatat	tgaarnacag	catcattaaa	rmgttwtktt	wttctccctt	420
gcaaaaaaca	tgtacngact	tcccgttgag	taatgccaa	ttgttttttt	tatnataaaa	480
cttgcccttc	attacatggt	tnaaagtggg	gtgggtggcc	aaaatattga	aatgatggaa	540
ctgactgata	aagctgtaca	aataagcagt	gtgcctaaca	agcaacacag	taatgttgac	600
atgcttaatt	cacaaatgct	aatttcatta	taaatgtttg	ctaaaataca	ctttgaacta	660
ttttctgtn	ttcccagagc	tgagatntta	gattttatgt	agtatnaagt	gaaaaantac	720
gaaaataata	acattgaaga	aaaananaaa	aaanaaaaaa	a		761

<210> 189

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

```

<400> 189
tttttttttt tttgccgatn ctactatntt attgcaggan gtgggggtgt atgcaccgca      60
caccgggggt atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca      120
aagccgcctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc      180
aaggcagggg ccaccagtcg aggggtggga atacaggggg tgggangtgt gcataagaag      240
tgataggcac agggcaccgc gtacagaccc ctgggtctct gacaggtnga ttctgaccag      300
gtcattgtgc cctgccagg cacagcgtn atctggaaaa gacagaatgc ttctcttttc      360
aaatttggct ngtcatngaa ngggcanttt tccaantng gctnggtctt ggtacncttg      420
gttcggccca gctcncgtc caaaaantat tcaccennct ccnaattgct tgcnggnecc      480
cc

```

```

<210> 190
<211> 471
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(471)
<223> n = A,T,C or G

```

```

<400> 190
tttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtggttttg      60
aaaactctcg catccagtga gaactacatt acaccacatt acagctngga atgtnctcca      120
aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag      180
cgctttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt      240
taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt      300
tgaaaaattt catgtatgca atccaaccaa agaacttnat tgggtgatcat gantnctcta      360
ctacatcnac cttgatcatt gccaggaacn aaaagtnnaa ancacnngt acaaaaanaa      420
tctgtaattn anttcaacct ccgtacngaa aaatnttnnt tataactcc c              471

```

```

<210> 191
<211> 402
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(402)
<223> n = A,T,C or G

```

```

<400> 191
gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct      60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa      120
attcttcacc agtcacatct tctaggacct ttttggatcc agttagtata agctcttcca      180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaagg aattyaattg      240
ctcgttctct aacaatgtcc tctccttgaa gtatttggct gaacaacca cctaaagtcc      300
ctttgtgcat ccatttttaa tatacttaat agggcattgk tncactaggt taaattctgc      360
aagagtcatc tgtctgcaaa agttgcgtta gtatatctgc ca              402

```

```

<210> 192
<211> 601
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

```

<222> (1)...(601)

<223> n = A,T,C or G

<400> 192

gagctcggat	ccaataatct	ttgtctgagg	gcagcacaca	tatncagtgc	catggnaact	60
ggctctacccc	acatgggagc	agcatgccgt	agntatataa	ggtcattccc	tgagtcagac	120
atgcytyttt	gaytaccgtg	tgccaagtgc	tggtgattct	yaacacacyt	ccatcccgyt	180
cttttgtgga	aaaactggca	cttkcttgga	actagcarga	catcacttac	aaattcaccc	240
acgagacact	tgaaaggtgt	aacaaagcga	ytcttgcat	gctttttgtc	cctccggcac	300
cagttgtcaa	tactaaccgc	ctggtttgcc	tccatcacat	ttgtgatctg	tagctctgga	360
tacatctcct	gacagtactg	aagaacttct	tcttttgttt	caaaagcarg	tcttggtgcc	420
tgttggatca	ggttcccatt	tcccagtcyg	aatgttcaca	tggcataatt	wacttcccac	480
aaaacattgc	gatttgaggc	tcagcaacag	caaatcctgt	tccggcattg	gctgcaagag	540
cctcgatgta	gccggccagc	gccaaggcag	gcgccgtgag	ccccaccagc	agcagaagca	600
g						601

<210> 193

<211> 608

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(608)

<223> n = A,T,C or G

<400> 193

atacagccca	natcccacca	cgaagatgcg	cttggtgact	gagaacctga	tgccggtcact	60
ggccccgctg	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgactctcytt	120
cccaacgcag	gcagmagcgg	gsccgggtcaa	tgaactccay	tcgtggett	gggtkgacgg	180
tkaagtgcag	gaagaggctg	accacctcgc	ggccaccag	gatgcccag	tggtcgggag	240
ctgcagcgaa	actcctcgat	ggatcatgagc	gggaagcgaa	tgaggcccag	ggccttgccc	300
agaaccttcc	gcctgtttct	tgccgtcacc	tgcatgtgct	gccgctgaca	ctcggcctcg	360
gaccagcgga	caaacggcrt	tgaacagccg	cacctcacgg	atgccagtg	tgctcgctc	420
caggammgsc	accagcgtgt	ccaggtcaat	gtcgggtgaag	ccctccgcgg	gtrattggcgt	480
ctgcagtgtt	tttgtcgatg	ttctccaggc	acaggtggc	cagctgcggg	tcategaaga	540
gtcgcgctg	cgtgagcagc	atgaaggcgt	tgctggctcg	cagttcttct	tcaggaactc	600
cacgcaat						608

<210> 194

<211> 392

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 194

gaacggctgg	accttgctc	gcattgtgct	tgctggcagg	gaataccttg	gcaagcagyt	60
ccagtcagag	cagccccaga	ccgctgccgc	ccgaagctaa	gcctgcctct	ggccttcccc	120
tccgcctcaa	tgagaacca	gtagtgggag	cactgtgttt	agagttaaga	gtgaacactg	180
tttgatttta	cttggaatt	tcctctgtta	tatagctttt	cccaatgcta	atttccaaac	240
aacaacaaca	aaataacatg	tttgccgtgt	aagttgtata	aaagtaggtg	attctgtatt	300
taaagaaaat	attactgtta	catatactgc	ttgcaatttc	tgtattttatt	gktnctstgg	360
aaataaatat	agttattaaa	ggtgtgcant	cc			392

<210> 195
 <211> 502
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(502)
 <223> n = A,T,C or G

<400> 195
 ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg 60
 ccgagctgag gcagatgttc ccacagtgc cccagagacc stgggstata gtytctgacc 120
 cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc 180
 aaggggaaggc cccattccgg ggstgttccc cgaggaggaa ggggaaggggc tctgtgtgcc 240
 ccccasgagg aagaggccct gagtcctggg atcagacacc ccttcacgtg tatccccaca 300
 caaatgcaag ctcaccaagg tcccctctca gtccccttcc stacaccctg amcggccact 360
 gscscacacc caccagagc acgccaccgc ccatggggar tgtgtcaag gartcgcngg 420
 gcarcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt 480
 gctnanaaaa aaaaanaaaa aa 502

<210> 196
 <211> 665
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(665)
 <223> n = A,T,C or G

<400> 196
 ggttacttgg ttctattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60
 cctctggaag ccttgcgag agcggacttt gtaattgttg gagaataact gctgaatttt 120
 wagctgtttk gaggttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga 180
 actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkatc 240
 aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt 300
 attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact 360
 tcacttgggt attttattgt aaatgartta caaaattctt aatttaagar aatggatgtg 420
 watatttatt tcattaattt ctttcctkgt ttacgtwaat tttgaaaaga wtgcgatgatt 480
 tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt 540
 ttcttagaat gtataaagggt ttagcccat cnaacttcaa agaaaaaat gaccacatac 600
 ttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan 660
 aagtg 665

<210> 197
 <211> 492
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(492)
 <223> n = A,T,C or G

<400> 197
 ttttnttttt ttttttttgc aggaaggatt ccattttattg tggatgcatt ttcacaatat 60
 atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg 120

aaggcagatt	cacagaacat	gctngtcngc	ttgcagtttt	acctcgtana	gatnacagag	180
aattatagtc	naaccagtaa	acnaggaatt	tactttttcaa	aagattaaat	ccaaactgaa	240
caaaattcta	ccctgaaact	tactccatcc	aaatattgga	ataanagtca	gcagtgatac	300
attctcttct	gaacttttaga	ttttctagaa	aaatatgtaa	tagtgatcag	gaagagctct	360
tgttcaaaag	tacaacnaag	caatgttccc	ttaccatagg	ccttaattca	aactttgatc	420
catttcactc	ccatcacggg	agtcaatgct	acctggggaca	cttgatattt	gttcatnctg	480
ancntggctt	aa					492

<210> 198
<211> 478
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(478)
<223> n = A,T,C or G

tttnttttgn	atttcantct	gtannaanta	ttttcattat	gtttattana	aaaatatnaa	60
tgtntccacn	acaaatcatn	ttacntnagt	aagaggccan	ctacattgta	caacatacac	120
tgagtatatt	ttgaaaagga	caagtttaaa	gtanacncat	attgccganc	atancacatt	180
tatacatggc	ttgattgata	tttagcacag	canaaactga	gtgagttacc	agaaanaaat	240
natatatgtc	aatcngattt	aagatacaaa	acagatccta	tggtacatan	catcntgtag	300
gagttgtggc	tttatgttta	ctgaaagtca	atgcagttcc	tgtacaaaga	gatggccgta	360
agcattctag	tacctctact	ccatgggttaa	gaatcgta	cttatgttta	catatgtnta	420
gggtaagaat	tgtgttaagt	naanttatgg	agaggtccan	gagaaaaatt	tgatncaa	478

<210> 199
<211> 482
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

agtgacttgt	cctccaacaa	aacccttga	tcaagtttgt	ggcactgaca	atcagaccta	60
tgctagtcc	tgtcatctat	tcgctactaa	atgcagactg	gaggggacca	aaaaggggca	120
tcaactccag	ctggattatt	ttggagcctg	caaactctatt	cctacttgta	cggactttga	180
agtgattcag	tttctctctac	ggatgagaga	ctggctcaag	aatatcctca	tcagacttta	240
tgaagccnac	tctgaacacg	ctggttatct	nagatgagaa	ncagagaaat	aaagtcnaga	300
aaatttacct	ggangaaaag	aggctttngg	ctggggacca	tccattgaa	ccttctctta	360
anggacttta	agaanaaact	accacatgtn	tgtngtatcc	tggtgccngg	ccgtttantg	420
aacntngacn	ncacccttnt	ggaatanant	cttgacngcn	tectgaactt	gtcctctgc	480
ga						482

<210> 200
<211> 270
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(270)
<223> n = A,T,C or G

<400> 200

cggccgcaag	tgcaactcca	gctggggccg	tgcggacgaa	gattctgcca	gcagttggtc	60
cgactgcgac	gacggcggcg	gcgacagtcg	caggtgcagc	gcgggcgcct	ggggtcttgc	120
aaggctgagc	tgacgccgca	gaggtegtgt	cacgtcccac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccggg	gaangcggga	ggcctcgggg	agcccctcgg	gaagggcggc	240
ccgagagata	cgcaggtgca	ggtggccgcc				270

<210> 201

<211> 419

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(419)

<223> n = A,T,C or G

<400> 201

tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttattttgca	60
gctagcaagg	taacagggtg	gggcatgggt	acatgttcag	gtcaacttcc	tttgtcgtgg	120
ttgattgggt	tgtctttatg	ggggcggggt	ggggtagggg	aaancgaagc	anaantaaca	180
tggagtgggt	gcaccctccc	tgtagaacct	ggttacnaaa	gcttggggca	gttcacctgg	240
tctgtgaccg	tcattttctt	gacatcaatg	ttattagaag	tcaggatatc	ttttagagag	300
tccactgtnt	ctggaggggg	attagggttt	cttgccaana	tccaancaaa	atccacntga	360
aaaagtgtga	tgatncangt	acngaatacc	ganggcatan	ttctcatant	cggtggcca	419

<210> 202

<211> 509

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(509)

<223> n = A,T,C or G

<400> 202

tttntttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
tggcacttaa	tccattttta	tttcaaaatg	tctacaaaant	ttnaatncnc	cattatacng	120
gtnattttnc	aaaatctaaa	nnttattcaa	atntnagcca	aantccttac	ncaaatnnaa	180
tacncncaaa	aatcaaaaat	atacntntct	ttcagcaaac	ttngttacat	aaattaaaaa	240
aatatatacg	gctgggtgtt	tcaaagtaca	attatcttaa	cactgcaaac	atnttttnna	300
ggaactaaaa	taaaaaaaaa	cactnccgca	aagggttaaag	ggaacaacaa	attcntttta	360
caacancnnc	nattataaaa	atcatatctc	aaatcttagg	ggaatatata	cttcacacng	420
ggatcttaac	ttttactnca	ctttgtttat	ttttttanaa	ccattgtntt	gggccaacaa	480
caatggnaat	nccnccnnc	tgactagt				509

<210> 203

<211> 583

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(583)

<223> n = A,T,C or G

<400> 203

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaatggaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgcttaaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaat	tatctaattc	ttccattttt	tccctattcc	aagtcaattt	300
gctttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaca	ggaagagana	atggcacaca	aaacaaacat	tttatattca	tatttctacc	420
tacgttaata	aaatagcatt	ttgtgaagcc	agctcaaaag	aaggcttaga	tccttttatg	480
tccatttttag	tcactaaacg	atatcnaaag	tgccagaatg	caaaagggtt	gtgaacattt	540
attcaaaagc	taatataaga	tatttcacat	actcatcttt	ctg		583

<210> 204

<211> 589

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(589)

<223> n = A,T,C or G

<400> 204

ttttttttnt	tttttttttt	ttttttntct	ttcttttttt	ttganaatga	ggatcgagtt	60
tttactcttc	tagatagggc	atgaagaaaa	ctcatctttc	cagctttaaa	ataacaatca	120
aatctcttat	gctatatcat	attttaagtt	aaactaatga	gtcactggct	tatcttctcc	180
tgaaggaaat	ctgttcattc	ttctcattca	tatagttata	tcaagtacta	ccttgcatat	240
tgagaggttt	ttcttctcta	tttacacata	tatttccatg	tgaatttgta	tcaaaccctt	300
attttcatgc	aaactagaaa	ataatgtntt	cttttgcata	agagaagaga	acaatatnag	360
cattacaaaa	ctgctcaaat	tgtttggtta	gnttatccat	tataattagt	tnggcaggag	420
ctaatacaaa	tcacattttac	ngacnagcaa	taataaaaact	gaagtaccag	ttaaatatcc	480
aaaataatta	aaggaacatt	tttagcctgg	gtataattag	ctaattcact	ttacaagcat	540
ttattnagaa	tgaattcaca	tgttattatt	ccntagccca	acacaatgg		589

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(545)

<223> n = A,T,C or G

<400> 205

ttttnttttt	ttttttcagt	aataatcaga	acaatattta	tttttatatt	taaaattcat	60
agaaaagtgc	cttacattta	ataaaagttt	gtttctcaaa	gtgatcagag	gaattagata	120
tngtcttgaa	caccaatatt	aatttgagga	aaatacacca	aaatacatta	agtaaattat	180
ttaagatcat	agagcttgta	agtgaaga	taaaatttga	cctcagaaac	tctgagcatt	240
aaaaatccac	tattagcaaa	taaattacta	tggaacttct	gctttaattt	tgtgatgaat	300
atgggggtgtc	actggtaaac	caacacattc	tgaaggatag	attacttagt	gatagattct	360
tatgtacttt	gctanatinac	gtggatatga	gttgacaagt	ttctctttct	tcaatctttt	420
aaggggcnga	ngaaatgagg	aagaaaagaa	aaggattacg	catactgttc	tttctatngg	480
aaggattaga	tatgtttcct	ttgccaatat	taaaaaaata	ataatgttta	ctactagtga	540
aaccc						545

<210> 206

<211> 487

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(487)

<223> n = A,T,C or G

<400> 206

tttttttttt	tttttttagtc	aagttttctna	tttttattat	aattaaagtc	ttggtcattt	60
catttattag	ctctgcaact	tacatattta	aattaaagaa	acgttnttag	acaactgtna	120
caatttataa	atgtaagggtg	ccattattga	gtanatatat	tcctccaaga	gtggatgtgt	180
cccttctccc	accaactaat	gaancagcaa	cattagttta	attttattag	tagatnatac	240
actgctgcaa	acgctaattc	tcttctccat	ccccatgtng	atattgtgta	tatgtgtgag	300
ttggtnagaa	tgcatacanca	atctnacaat	caacagcaag	atgaagctag	gcntgggctt	360
tcggtgaaaa	tagactgtgt	ctgtctgaat	caaatgatct	gacctatcct	cgggtggcaag	420
aactcttcga	accgcttcct	caaaggcngc	tgccacattt	gtggcntctn	ttgcacttgt	480
ttcaaaa						487

<210> 207

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 207

tgaattggct	aaaagactgc	atttttanaa	ctagcaactc	ttatttcttt	cctttaaaaa	60
tacatagcat	taaatcccaa	atcctattta	aagacctgac	agcttgagaa	ggctactact	120
gcatttatag	gaccttctgg	tggttctgct	gttacntttg	aantctgaca	atccttgana	180
atccttgcat	gcagaggagg	taaaaggat	tggattttca	cagaggaana	acacagcgca	240
gaaatgaagg	ggccaggctt	actgagcttg	tccactggag	ggctcatggg	tgggacatgg	300
aaaagaaggc	agcctaggcc	ctggggagcc	ca			332

<210> 208

<211> 524

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(524)

<223> n = A,T,C or G

<400> 208

agggcggtgt	gcggaggggc	ttactgtttt	gtctcagtaa	caataaatac	aaaaagactg	60
gttgtgttcc	ggcccccacc	aaccacgaag	ttgattttct	tttgtgtcag	agtgactgat	120
tttaaaggac	atggagcttg	tcacaatgtc	acaatgtcac	agtgtgaagg	gcacactcac	180
tcccgcgtga	ttcacattta	gcaaccaaca	atagctcatg	agtccatact	tgtaaatact	240
tttggcagaa	tacttnttga	aacttgacga	tgataactaa	gatccaagat	atttcccaaa	300
gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagcccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgtcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcaatc	atctatccaa	480
aaaccattac	ctgatccact	tccggtaatg	caccaccttg	gtga		524

<210> 209
<211> 159
<212> DNA
<213> Homo sapien

<400> 209
gggtgaggaa atccagagtt gccatggaga aaattccagt gtcagcattc ttgctccttg 60
tggccctctc ctacactctg gccagagata ccacagtcaa acctggagcc aaaaaggaca 120
caaaggactc tcgacccaaa ctgccccaga ccctctcca 159

<210> 210
<211> 256
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (256)
<223> n = A,T,C or G

<400> 210
actccctggc agacaaaggc agaggagaga gctctgtag ttctgtgttg ttgaactgcc 60
actgaatttc tttccacttg gactattaca tgccantga gggactaatg gaaaaacgta 120
tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180
ttgcaggggtg naaatgggan ggctggtttg ttanatgaac agggacatag gaggtaggca 240
ccaggatgct aatatca 256

<210> 211
<211> 264
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (264)
<223> n = A,T,C or G

<400> 211
acattgtttt tttgagataa agcattgaga gagctctcct taacgtgaca caatggaagg 60
actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
atattcaagc acatatgtta tatattatc agttccatgt ttatagccta gttaaggaga 180
ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga 240
aaaaaaggag caaatgagaa gcct 264

<210> 212
<211> 328
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (328)
<223> n = A,T,C or G

<400> 212
acccaaaaat ccaatgctga atatttggt tcattattcc canattcttt gattgtcaaa 60
ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120
gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180

ttnaatttca ttccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta	240
cccctacnac tctttactct ctgganaggg ccagtgggtg tagctataag cttggccaca	300
tttttttttc ctttattcct ttgtcaga	328

<210> 213
 <211> 250
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(250)
 <223> n = A,T,C or G

<400> 213	
acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt	60
taaagcattg ctcaactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgccca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatata tctctnacct	240
tctcatcggt	250

<210> 214
 <211> 444
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(444)
 <223> n = A,T,C or G

<400> 214	
accagaatc caatgctgaa tatttggtt cattattccc agattctttg attgtcaaag	60
gatttaagt tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg	120
tttatatatg cagcaacaat attcaagcgc gacaacaggc tattgaactt gcccgccagt	180
tgaatttcat tccattgac ttgggactct tatcatcagc canagagatt gaaaatttac	240
ccctacgact ctttactctc tggagagggc cagtgggtgt agctataagc ttggccacat	300
ttttttttcc tttattcctt tgtcagagat gcgattcctc catatgctan aaaccaacag	360
agtgactttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt	420
actttgtctt ccctaataata cctc	444

<210> 215
 <211> 366
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(366)
 <223> n = A,T,C or G

<400> 215	
acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt	60
taaagcattg ctcaactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgccca aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatata tctctgacct	240
tctcatcggt aagcagaggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa	300
tccaagctgt tttctacact gtaaccaggt ttccaaccaa ggtggaaatc tcctatactt	360

ggtgcc

366

<210> 216
<211> 260
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(260)
<223> n = A,T,C or G

<400> 216
ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60
caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120
taataaaaag tnnaaaaggc ctctttctcaa cttttttccc ttnggctgga aaatttaaaa 180
atcaaaaatt tcttnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240
aattcttctt tccctctttt 260

<210> 217
<211> 262
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(262)
<223> n = A,T,C or G

<400> 217
acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60
tcttgcttat aattttctat tttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120
ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180
atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240
atatacttca tgcttgtaaa gt 262

<210> 218
<211> 205
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(205)
<223> n = A,T,C or G

<400> 218
accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60
cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaagactc 120
aggcctcccc agttctactg acctttgtcc ttangtntna ngtcagggt tgctaggaaa 180
anaaatcagc agacacaggt gtaaa 205

<210> 219
<211> 114
<212> DNA
<213> Homo sapien

<400> 219

tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60
accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220
<211> 93
<212> DNA
<213> Homo sapien

<400> 220
actagccagc acaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta 60
aaataagcat ttagtgctca gtccctactg agt 93

<210> 221
<211> 167
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(167)
<223> n = A,T,C or G

<400> 221
actangtgca ggtgcgcaca aatatttgct gatattccct tcactcttga ttccatgagg 60
tcttttgccc agcctgtggc tctactgtag taagtctctg ctgatgagga gccagnatgc 120
ccccactac cttccctgac gctccccana aatcacccaa cctctgt 167

<210> 222
<211> 351
<212> DNA
<213> Homo sapien

<400> 222
agggcgtggt gcggagggcg gtactgacct ctagtaggagg aggatgcatt ctggcacc 60
gttcttcacc tgtcccccaa tcttataaag gccatactgc ataaagtcaa caacagataa 120
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240
taggtgagca tgattagaga gcttgtaggt tgcttttaca tatatctggc atatttgagt 300
ctcgatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t 351

<210> 223
<211> 383
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 223
aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat 60
tggttaattat ggtcaattta atwrtrttkt ggggcatttc cttacattgt cttgacaaga 120
ttaaagtgtc tgtgccaaaa ttttgatttt tttttggaga cttcttatca aaagtaatgc 180
tgccaaagga agtctaagga attagtagtg ttcccmtcac ttgtttggag tgtgctatcc 240
taaaagattt tgatttctct gaatgacaat tatattttta ctttggtggg ggaaanagtt 300
ataggaccac agtcttcact tctgatactt gttaaattaat cttttattgc acttgttttg 360
accattaagc tatatgttta aaa 383

<210> 224
 <211> 320
 <212> DNA
 <213> Homo sapien

<400> 224
 cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60
 aaaagtttgt gacattgtag tagggagtgt gtacccttta ctcccatca aaaaaaaat 120
 ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa 180
 gagaaaatac tactttctcr aaatggaagc ctttaaagggt gctttgatac tgaaggacac 240
 aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgcaat 300
 tttaractcm gcattgtgac 320

<210> 225
 <211> 1214
 <212> DNA
 <213> Homo sapien

<400> 225
 gaggactgca gccgcactc gcagccctgg caggcggcac tggatcatgga aaacgaattg 60
 ttctgctcgg gcgtcctggg gcatccgcag tgggtgctgt cagccgcaca ctgtttccag 120
 aactcctaca ccacggggt gggcctgcac agtcttgagg ccgaccaaga gccaggggagc 180
 cagatgggtg aggcagcct ctccgtacgg caccagagt acaacagacc ctgtctcgct 240
 aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300
 atcagcattg cttgcagtg ccctaccgag gggaactctt gcctcgtttc tggctggggg 360
 ctgctggcga acggcagaat gctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct 420
 gaggaggtct gcagtaagct ctatgaccgg ctgtaccacc ccagcatgtt ctgcgcgggc 480
 ggagggcaag accagaagga ctccctgcaac ggtgactctg gggggcccct gatctgcaac 540
 gggactctgc agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcca 600
 ggtgtctaca ccaacctctg caaattcact gactggatag agaaaaccgt ccaggccagt 660
 taactctggg gactgggaac ccatgaaatt gacccccaaa tacatcctgc ggaaggaatt 720
 caggaataac tgttccagc ccctcctccc tcaggcccag gactccaggc cccagcccc 780
 tctcctcctca aaccaagggt acagatcccc agccccctct ccctcagacc caggagtcca 840
 gacccccag cccctcctcc ctccagacca ggagtcacgc ccctcctccc tcagaccagc 900
 gactccagac cccccagccc ctccctcctc agaccaggg gtccaggccc ccaaccctc 960
 ctccctcaga ctccagaggtc caagccccca accctcctt cccagaccc agaggtccag 1020
 gtcccagccc ctccctcctc agaccagcg gtccaatgcc acctagactc tccctgtaca 1080
 cagtgcctcc ttgtggcagc ttgacccaac cttaccagtt ggtttttcat tttttgtccc 1140
 ttcccttag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaaaaaaaa aaaa 1214

<210> 226
 <211> 119
 <212> DNA
 <213> Homo sapien

<400> 226
 acccagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa 60
 agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227
 <211> 818
 <212> DNA
 <213> Homo sapien

<400> 227
 acaattcata gggacgacca atgaggacag ggaatgaacc cggtctctccc ccagccctga 60

tttttgctac	atatgggggc	ccttttcatt	ctttgcaaaa	acactggggtt	ttctgagaac	120
acggacgggtt	cttagcacaa	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttcctc	ctctggagga	aaggtgggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgtcgggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgtcccc	ttccaatcag	ccacttctga	gaacccccat	ctaacttcct	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaagggtg	caccctcagc	agagaagccg	agagcttaac	tctggctcgt	tccagagaca	480
acctgctggc	tgtcttggga	tgcgcccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcatgagagg	600
gacaggctct	gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggct	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818

<210> 228

<211> 744

<212> DNA

<213> Homo sapien

<400> 228

actggagaca	ctgttgaact	tgatcaagac	ccagaccacc	ccaggtctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaaacga	gcctcctcct	tgggaagatgg	aagaccgtgt	120
tctgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gcgagtcac	atttcaatgg	180
taggaaaagt	ggcttcgtaa	aatagaagag	cagtcactgt	ggaactacca	aatggcgaga	240
tgtcgggtgc	acattgggggt	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggcagttt	gttccactga	agcttttccc	acagcagtc	acctctgcag	360
gctggcagct	gaatggcctg	ccggtggctc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	gttggctcct	tccaggttgg	480
ccagacggtg	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctgggtga	cagtgacccg	540
ccgtgggtatg	ccttggccca	ttccagcagt	cccagttatg	catttcaagt	ttgggggttg	600
ttcttttctg	taatgttctc	ctgtgttgct	agctgtcttc	atttctctggg	ctaagcagca	660
ttgggagatg	tggaccagag	atccactcct	taagaaccag	tggcgaaaga	cactttcttt	720
cttcaactctg	aagtagctgg	tggt				744

<210> 229

<211> 300

<212> DNA

<213> Homo sapien

<400> 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatccaaa	tcatgtgaac	60
cattacacat	cgaaataaaa	gaaaggtggc	agacttgccc	aacgccaggc	tgacatgtgc	120
tgcagggttg	ttgtttttta	attattattg	ttagaaacgt	caccacagc	ccctgttaat	180
ttgtatgtga	cagccaactc	tgagaaggtc	ctatttttcc	acctgcagag	gatccagtct	240
cactaggtc	ctccttgccc	tcacactgga	gtctcgcgca	gtgtgggtgc	ccactgacat	300

<210> 230

<211> 301

<212> DNA

<213> Homo sapien

<400> 230

cagcagaaca	aatacaaaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120
caatataaag	tcttggttca	cactcaggaa	cgagagctga	cccagttaag	ggagaagttg	180
cgggaaggga	gagatgcctc	cctctcattg	aatgagcatc	tccaggccct	cctcactccg	240
gatgaaccgg	acaagtccca	ggggcaggac	ctccaagaaa	cagacctcgg	ccgcgaccac	300
g						301

<210> 231
<211> 301
<212> DNA
<213> Homo sapien

<400> 231
gcaagcacgc tggcaaatct ctgtcaggtc agctccagag aagccattag tcatttttagc 60
caggaactcc aagtccacat ccttggcaac tggggacttg cgcaggttag ccttgaggat 120
ggcaacacgg gactttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg 180
tctgaggatg gcaggatcaa tgatgtcagg ccggttggtg ccgccaatga tgaacacatt 240
tttttttgtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc 300
c 301

<210> 232
<211> 301
<212> DNA
<213> Homo sapien

<400> 232
agtaggtatt tcgtgagaag ttcaacacca aaactggaac atagttctcc ttcaagtgtt 60
ggcgacacgc gggcttctctg attctggaat ataactttgt gtaaattaac agccacctat 120
agaagagtcc atctgctgtg aaggagagac agagaactct gggttccgtc gtcctgtcca 180
cgtgctgtac caagtgtctg tgccagcctg ttacctgttc tcaactgaaa tctggctaata 240
gctcttgtgt atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact 300
g 301

<210> 233
<211> 301
<212> DNA
<213> Homo sapien

<400> 233
atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag 60
atgctaaggc cccagagatc gtttgatcca accctcttat ttccagaggg gaaaatgggg 120
cctagaagtt acagagcatc tagctggtgc gctggcacc cttggcctcac acagactccc 180
gagtagctgg gactacaggc acacagtcac tgaagcaggc cctgttagca attctatgag 240
tacaaattaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa 300
c 301

<210> 234
<211> 301
<212> DNA
<213> Homo sapien

<400> 234
aggctcctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga 60
cattttattc atcatgatgc tttcttttctg ttcttctttt cgttttcttc tttttctttt 120
tcaatttcag caacatactt ctcaatttct tcaaggattta aaatcttgag ggattgatct 180
cgctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgc 240
ttgatcacca gcttaatggg cagatcatct gcttcaatgg cttcgtcagt atagttcttc 300
t 301

<210> 235
<211> 283
<212> DNA
<213> Homo sapien

<400> 235

tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg	60
aattccctca tcttttaggg aatcatttac caggtttgga gaggattcag acagctcagg	120
tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata	180
atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatcaaca	240
ttagggattc aaagaaatat tagatttaag ctcacactgg tca	283

<210> 236

<211> 301

<212> DNA

<213> Homo sapien

<400> 236

aggtcctcca ccaactgcct gaagcacggt taaaattggg aagaagtata gtgcagcata	60
aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg	120
tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatag	180
tgggtagacg gcttcatgag tacagtgtac tgtggatcgc taatctggac ttgggttgta	240
aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc	300
a	301

<210> 237

<211> 301

<212> DNA

<213> Homo sapien

<400> 237

cagtggtagt ggtggtggac gtggcggttg tegtgggtgcc ttttttggtg cccgtcacaa	60
actcaatttt tgttcgctcc tttttggcct tttccaattt gtccatctca attttctggg	120
ccttggtctaa tgctcatag taggagtcct cagaccagcc atggggatca aacatatcct	180
ttgggtagtt ggtgccaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaatcta	240
gggttccgaa attcttttct cctttggata atgtagttca tatccattcc ctcctttatc	300
t	301

<210> 238

<211> 301

<212> DNA

<213> Homo sapien

<400> 238

gggcagggtt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt	60
gttcacagtt cagccccctg ctcagaaaac caacgggcca gctaaggaga ggaggaggca	120
ccttgagact tcggagtcg aggcctctcca gggttcccca gcccatcaat cattttctgc	180
acccccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca	240
gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aatttcttta	300
t	301

<210> 239

<211> 239

<212> DNA

<213> Homo sapien

<400> 239

ataagcagct aggaattct ttatttagta atgtcctaac ataaaagtgc acataactgc	60
ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa	120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgccg gcatacacag tatacaggtc cttcaggga	239

<210> 240

<211> 300
<212> DNA
<213> Homo sapien

<400> 240
ggctcctaattg aagcagcagc ttccacattt taacgcaggt ttacgggtgat actgtccttt 60
gggatctgcc ctccagtga accttttaag gaagaagtgg gcccaagcta agttccacat 120
gctgggtgag ccagatgact tctgttcctt ggtcactttc ttcaatgggg cgaatggggg 180
ctgccaggtt tttaaaatca tgcttcattt tgaagcacac ggtcacttca cctcctcac 240
gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc 300

<210> 241
<211> 301
<212> DNA
<213> Homo sapien

<400> 241
gaggtctggg gctgaggtct ctgggctagg aagaggagtt ctgtggagct ggaagccaga 60
cctcttttga ggaactcca gcagctatgt tgggtgtctt gagggaatgc aacaaggctg 120
ctcctccatg tattggaaaa ctgcaaactg gactcaactg gaaggaagtg ctgctgccag 180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct 240
tctcctcct gtcatacggg ctctctcaag cactccttgt tgtcaggggc ctaaaaggga 300
g 301

<210> 242
<211> 301
<212> DNA
<213> Homo sapien

<400> 242
ccgaggtcct gggatgcaac caatcactct gtttcacgtg actttttatca ccatacaatt 60
tgtggcattt cctcattttc tacattgtag aatcaagagt gttaaataaat gtatatcgat 120
gtcttcaaga atatatcatt cctttttcac tagaaccat tcaaaatata agtcaagaat 180
cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta 240
taagtaccca aagttttata aatcaaaaagc cctaattgata accattttta gaattcaatc 300
a 301

<210> 243
<211> 301
<212> DNA
<213> Homo sapien

<400> 243
aggtaagtcc cagtttgaag ctcaaaagat ctggtatgag cataggctca tcgacgacat 60
ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg 120
tgacgtgcag tcggactctg tggcccaagg gtatggctct ctcggcatga tgaccagcgt 180
gctggtttgt ccagatggca agacagtaga agcagaggct gccacggga ctgtaaccgg 240
tcactaccgc atgttcaga aaggacagga gacgtccacc aatccattg cttccatttt 300
t 301

<210> 244
<211> 300
<212> DNA
<213> Homo sapien

<400> 244
gctggtttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa 60
gtcatgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc 120

ccagggacct	tggaaacagt	tgacactgta	agggtgcttgc	tccccaagac	acatcctaaa	180
agggtgtgta	atgggtgaaa	cgtcttccct	ctttattgcc	ccttcttatt	tatgtgaaca	240
actgtttgc	ttttgtgtat	cttttttaaa	ctgtaaagtt	caattgtgaa	aatgaatata	300

<210> 245
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 245						
gtctgagtat	ttaaaatggt	attgaaatta	tccccaacca	atgttagaaa	agaaagaggt	60
tatatactta	gataaaaaat	gagggtgaatt	actatccatt	gaaatcatgc	tcttagaatt	120
aaggccagga	gatattgtca	ttaatgtara	cttcaggaca	ctagagtata	gcagccctat	180
gttttcaaag	agcagagatg	caattaaata	ttgttttagca	tcaaaaaggc	cactcaatac	240
agctaataaa	atgaaagacc	taattttctaa	agcaattctt	tataattttac	aaagttttta	300
g						301

<210> 246
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 246						
ggtctgtcct	acaatgcctg	cttcttgaaa	gaagtcggca	ctttctagaa	tagctaaata	60
acctgggctt	atttttaaaga	actatttgta	gctcagattg	gttttccctat	ggctaaaata	120
agtgtctctt	gtgaaaatta	aataaaacag	ttaattcaaa	gccttgatat	atgttaccac	180
taacaatcat	actaaatata	ttttgaagta	caaagtttga	catgctctaa	agtgacaacc	240
caaatgfgtc	ttacaaaaca	cgttcctaac	aaggatatgct	ttacactacc	aatgcagaaa	300
c						301

<210> 247
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 247						
aggtcctttg	gcagggtctca	tggatcagag	ctcaaactgg	agggaaaggc	atttcgggta	60
gcctaagagg	gcgactggcg	gcagcacaac	caaggaaggc	aagggtgttt	ccccacgct	120
gtgtcctgtg	ttcagggtgcg	acacacaatc	ctcatgggaa	caggatcacc	catgcgctgc	180
ccttgatgat	caagggttggg	gcttaagtgg	attaagggag	gcaagttctg	ggttccttgc	240
cttttcaaac	catgaagtca	ggctctgtat	ccctcctttt	cctaactgat	attctaacta	300
a						301

<210> 248
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 248						
aggtccttgg	agatgccatt	tcagccgaag	gactcttctw	ttcggaagta	caccctcact	60
attaggaaga	ttcttagggg	taatttttct	gaggaaggag	aactagccaa	cttaagaatt	120
acaggaagaa	agtgggttgg	aagacagcca	aagaaataaa	agcagattaa	attgtatcag	180
gtacattcca	gcctgttggc	aactccataa	aaacatttca	gatttttaac	ccgaatttag	240
ctaataagac	tggatttttg	ttttttatgt	tgtgtgtcgc	agagctaaaa	actcagttcc	300
c						301

<210> 249
 <211> 301

<212> DNA

<213> Homo sapien

<400> 249

```

gtccagagga agcacctggg gctgaactag gcttgccttg ctgtgaactt gcacttggag      60
ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgcgc      120
ccagggagac acagcagtga ctacagagctg gtgcacacct gtgcctccct cctcaccgcc      180
catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag      240
actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt      300
a                                                                                   301

```

<210> 250

<211> 301

<212> DNA

<213> Homo sapien

<400> 250

```

ggctctgtgac aaggacttgc aggcctgtggg aggcaagtga cccttaacac tacactttctc      60
cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc      120
cataagcaca tcagtacttt tctctggctg gaatagtaaa cttaaagtatg gtacatctac      180
ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta      240
caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc      300
a                                                                                   301

```

<210> 251

<211> 301

<212> DNA

<213> Homo sapien

<400> 251

```

gccgaggtcc tacatttggc ccagtttccc cctgcacccct ctccaggggc cctgectcat      60
agacaaccctc atagagcata ggagaactgg ttgccctggg gccaggggga ctgtctggat      120
ggcagggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct      180
cattggggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgga      240
cctctggagg ggggcagtgg aatcccagct ccaggacgga tctgtcgaag aagatatact      300
c                                                                                   301

```

<210> 252

<211> 301

<212> DNA

<213> Homo sapien

<400> 252

```

gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttctca      60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata      120
tcatttcttt ttacttagga acccattcaa aatataagtc aagaatctta atatcaacaa      180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taccctaaagt      240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc      300
a                                                                                   301

```

<210> 253

<211> 301

<212> DNA

<213> Homo sapien

<400> 253

```

ttccctaaga agatgttatt ttgttgggtt ttgttcccc tccatctcga ttctcgtacc      60
caactaaaaa aaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctcttagct      120

```

tggtctgatt gttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg	180
gatttttttt cttagagAAC cACAAAacat aaaaggagca agtcggactg aatacctgtt	240
tccatagtgc ccacagggtA ttcctcacat tttctccata ggaaaaatgct ttttcccaag	300
g	301

<210> 254
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 254	
cgctgcgcct ttccttggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg	60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc	120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa	180
gaaaaaaata aagctttgga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc	240
acttaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc	300
t	301

<210> 255
 <211> 302
 <212> DNA
 <213> Homo sapien

<400> 255	
agcttttttt ttttttttt ttttttttt ttcattaaaa aatagtgtc tttattataa	60
attactgaaa tgtttcttt ctgaatataa atataaatat gtgcaaagtt tgacttggat	120
tgggattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg	180
aggaaaaagg actggagggt gaatctttat aaaaaacaag agtgattgag gcagattgta	240
aacattatta aaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac	300
aa	302

<210> 256
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 256	
gttccagaaa acattgaagg tggttccca aagtctaact agggataccc cctctagcct	60
aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc	120
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat	180
aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt	240
gtggcctctc ggctgggtta gcaagaacat tcagggtagg cctaagttaa tcgtgttagt	300
t	301

<210> 257
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 257	
gttgtggagg aactctggct tgctcattaa gtctactga ttttcactat ccctgaatt	60
tccccactta tttttgtctt tcaactatcg aggccttaga agaggcttac ctgcctccag	120
tcttacctag tccagtctac ccctggagt tagaatggcc atcctgaagt gaaaagtaat	180

gtcacattac tcccttcagt gatttcttgt agaagtgcc atccctgaat gccaccaaga 240
tcttaattctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc 300
c 301

<210> 258
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 258
cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc 60
agggggccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg 180
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat 240
tggtgatccc tgggagcgcc ggtggagtaa cgttggtcca tggaaagcag cgcccacaac 300
t 301

<210> 259
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 259
tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg 60
gtgtcctgaa gtgatttgga cccctgaggg cagacaccta agtaggaatc ccagtgggaa 120
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtgggcccag gaagggtctgt 180
tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggctt 240
ccctcccac tctcaagca gtgtccttgt tgagccattt gcatecttgg ctccagggtg 300
c 301

<210> 260
<211> 301
<212> DNA
<213> Homo sapien

<400> 260
tttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaa at aagcaatggt 60
aaggtgtctt aacttgaaaa agattaggag tcaactgggtt acaagttata attgaatgaa 120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaacaa caggattaac 180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttaataaac agactgattc 240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca 300
c 301

<210> 261
<211> 301
<212> DNA
<213> Homo sapien

<400> 261

aaatattcga	gcaaactctg	taactaatgt	gtctccataa	aaggctttga	actcagtga	60
tctgcttcca	tccacgattc	tagcaatgac	ctctcggaca	tcaaagctcc	tcttaagggt	120
agcaccaact	attccatata	attcatcagc	aggaaataaa	ggctcttcag	aagggttcaat	180
ggtgacatcc	aattttcttct	gataatttag	attcctcaca	accttcctag	ttaagtgaag	240
ggcatgatga	tcacccaaag	cccagtggtc	acttactcca	gactttctgc	aatgaagatc	300
a						301

<210> 262

<211> 301

<212> DNA

<213> Homo sapien

<400> 262

gaggagagcc	tgttacagca	tttgtaagca	cagaatactc	caggagtatt	tgtaattgtc	60
tgtgagcttc	ttgccgcaag	tctctcagaa	atttaaaaag	atgcaaattcc	ctgagtcacc	120
cctagacttc	ctaaaccaga	tcctctgggg	ctggaacctg	gcactctgca	tttgtaatga	180
gggctttctg	gtgcacacct	aattttgtgc	atctttgccc	taaatacctgg	attagtgcgc	240
catcattacc	cccacattat	aatgggatag	attcagagca	gatactctcc	agcaaagaat	300
c						301

<210> 263

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 263

tttagcttgt	ggtaaatgac	tcacaaaact	gattttaaaa	tcaagttaat	gtgaattttg	60
aaaattacta	cttaatccta	attcacaata	acaatggcat	taagggttga	cttgagttgg	120
ttcttagtat	tattttatggt	aaataggctc	ttaccacttg	caaataactg	gccacatcat	180
taatgactga	cttcccagta	aggctctcta	aggggtaagt	angaggatcc	acaggatttg	240
agatgctaag	gccccagaga	tcgtttgatc	caacctctct	attttcagag	gggaaaatgg	300
g						301

<210> 264

<211> 301

<212> DNA

<213> Homo sapien

<400> 264

aaagacgtta	aaccactcta	ctaccacttg	tggaactctc	aaagggtaaa	tgacaaascc	60
aatgaatgac	tctaaaaaca	atatttacat	ttaatggttt	gtagacaata	aaaaaacaag	120
gtggatagat	ctagaattgt	aacattttta	gaaaaccata	scatttgaca	gatgagaaag	180
ctcaattata	gatgcaaagt	tataactaaa	ctactatagt	agtaaagaaa	tacatttcac	240
accttcata	taaattcact	atcttggctt	gaggcactcc	ataaaatgta	tcacgtgcat	300
a						301

<210> 265

<211> 301

<212> DNA

<213> Homo sapien

<400> 265

tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcattcttgt	60
cttcttgtga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta	120
catattcttg gaagtctcta atcaactttt gttccatttg tttcatttct tcaggaggga	180
ttttcagttt gtcaacatgt tctctaacaa cacttgccca tttctgtaaa gaatccaaag	240
cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg	300
c	301

<210> 266
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 266	
taccgtctgc ccttctctcc atccaggcca tctgogaate tacatgggtc ctctatttcg	60
acaccagatc actcttttct ctaccacag gcttgctatg agcaagagac acaacctcct	120
ctcttctgtg ttccagcttc ttttctgtt ctcccaccc cttaagttct attcctgggg	180
atagagacac caatacccat aacctctctc ctaagcctcc ttataaccca ggggtgcacag	240
cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgctg	300
a	301

<210> 267
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 267	
aaagagcaca ggccagctca gcttgccctg gccatctaga ctcagcctgg ctccatgggg	60
gttctcagtg ctgagtccat ccaggaaaag ctcacctaga ccttctgagg ctgaatcttc	120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgggtc ggagtaaagc	180
ctcattctga ttcctctcct tcttttctt caagttggct ttcctcacat ccctctgttc	240
aattcgcttc agcttgctg ctttagccct catttcacaga agcttcttct ctttggcatc	300
t	301

<210> 268
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 268	
aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta	60
gatcttggga gagctgggtc ttctaaggag aaggaggaag gacagatgta actttggatc	120
tcgaagagga agtctaattg aagtaattag tcaacggtcc ttgtttagac tcttgggaata	180
tgctgggtgg ctcagtggag ccttttggag aaagcaagta ttattcttaa ggagtaacca	240
cttcccatg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact	300
a	301

<210> 269
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 269	
taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat	60
aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact	120
atagtcacag accttaata ttcacattgt tttctatgtc tactgaaaat aagttcacta	180
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta	240
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc	300
t	301

<210> 270
<211> 301
<212> DNA
<213> Homo sapien

<400> 270
cattgaagag cttttgcgaa acatcagaac acaagtgtt ataaaattaa ttaagcctta 60
cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120
gagcttgctg gtgcagtgca tattggataa cactattcat ggccgaattg atcaagtcaa 180
ccaactcctt gaactggatc atcagaagaa ggggtggtgca cgatatactg cactagataa 240
tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300
a 301

<210> 271
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 271
aaaagggttct cataagatta acaattttaa taaatatattg atagaacatt ctttctcatt 60
tttatagctc atcttttagg ttgatattca gttcatgtt ccttgctgt tcttgatcca 120
gaattgcaat cacttcatca gcctgtatc gctccaattc tctataaagt gggccaagg 180
tgaaccacag agccacagca cactctttc ccttggtgac tgccttcacc ccatganggt 240
tctctctcc agatganaac tgatcatgcy cccacatttt gggttttata gaagcagtca 300
c 301

<210> 272
<211> 301
<212> DNA
<213> Homo sapien

<400> 272
taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaagtgc 60
ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga 120
tccaataatt cctcatgat gagcaagaaa aattctttgc gcacccctcc tgcattccaca 180
gcatcttctc caacaaatat aaccttgagt ggcttcttgc aatctatgtt cttgttttc 240
ctaaggactt ccattgcac tcctacaata ttttctctac gcaccactag aattaagcag 300
g 301

<210> 273
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 273
acatgtgtgt atgtgtatct ttgggaaan aanaagacat cttgtttayt atttttttgg 60
agagangctg ggacatggat aatcacwtaa ttgtctayta tyactttaat ctgactygaa 120

```

gaaccgtcta aaaataaaat ttaccatgtc dtatattcct tatagtatgc ttatttcacc 180
ttytttctgt ccagagagag tatcagtgac ananatttma ggggtgaamac atgmattggg 240
gggacttnty ttacngagm accctgcccg sgcgcctcg makcngantt ccgcsananc 300
t 301

```

```

<210> 274
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 274
cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg 60
aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa 120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttggt gaaaagtcca 180
tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc 240
aattgtgctt cttttgataa gaagctttct tggtcatatc aggaaattcc aganaaagtc 300
c 301

```

```

<210> 275
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 275
tcgggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60
gggtgaaatt ggccaacttt ctattaactt atgttggtgaa ttttgccacc aacagtaagc 120
tggecccttct aataaaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag 180
tcaagagact cccaggcctc agcgtacctg cccggggcggc cgctcgaagc cgaattctgc 240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccctat 300
a 301

```

```

<210> 276
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 276
tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat 60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tataaaaaat 120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180
caatacattt aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt 240
aaaactattc agtatgtttc ctttgcttca tgtctgagaa ggctctcctt caatggggat 300
g 301

```

```

<210> 277
<211> 301
<212> DNA
<213> Homo sapien

```

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 277
 tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60
 atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120
 gaatcatggc actcctgata ctttcccaa tcaacactct caatgcccc ccctcgtcct 180
 caccatagtg gggagactaa agtggccacg gatttgcctt anggtgtcag tgcgttctga 240
 gttcncctgtc gattacatct gaccagtctc ctttttccga agtcctccg ttcaatcttg 300
 c 301

<210> 278
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 278
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120
 cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180
 aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgtc tcacagggtt 240
 tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300
 c 301

<210> 279
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 279
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
 gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120
 ttagaccttt accttccagc caccacacag tgcttgatat ttcagagtca gtcattgggt 180
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
 a 301

<210> 280
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 280
 ggtactggag ttttccctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60
 tagaaaggtg gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct 120

tgagaaaaaa acctaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180
gtttgatata gtttaggggt gggggttagat taagatctaa attacatcag gacaaagaga 240
cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300
t 301

<210> 281
<211> 301
<212> DNA
<213> Homo sapien

<400> 281
agggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatatctc 60
gccgagcaat ccaaattcctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120
atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180
tgtgtagcac actgcgatta cagctaaata acccgatttt gtgtgtcatg tttgcatttc 240
tgacaagtga aacaggatct tacgatggag ttttztatga aaacaaagtt gcagtacctc 300
g 301

<210> 282
<211> 301
<212> DNA
<213> Homo sapien

<400> 282
cagggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60
tccagaaccc aaaaattaag aaattcaaaa agacattttg tgggcacctg ctagcacaga 120
agcgcagaag caaagcccag gcagaacat gtaacctta cagctcagcc tgcacagaag 180
cgcagaagca aagcccaggc agaaccatgc taaccttaca gctcagcctg cacagaagcg 240
cagaagcaaa gccccaggcag aacatgctaa cttacagct cagcctgcac agaagcacag 300
a 301

<210> 283
<211> 301
<212> DNA
<213> Homo sapien

<400> 283
atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaaag 60
cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120
gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat ttttctatc 180
acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcattcttta 240
ggaaacatat acatttttaa aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300
g 301

<210> 284
<211> 301
<212> DNA
<213> Homo sapien

<400> 284
cagggtacaaa acgctattaa gtggcttaga atttgaacat ttgtggtctt tatttacttt 60
gcttcgtgtg tgggcaaagc aacatcttcc ctaaataatat attaccaaga aaagcaagaa 120
gcagattagg tttttgacaa aacaaacagg ccaaagggg gctgacctgg agcagagcat 180
ggtgagaggc aaggcatgag agggcaagtt tggtgtggac agatctgtgc ctactttatt 240
actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gtagaaatt 300
a 301

<210> 285

<211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 285
 acatcaccat gatcggatcc cccacccatt atacgttgta tgtttacata aatactcttc 60
 aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac 120
 caggaaagca aatgctatct acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180
 attaaatatt tctgacttct tttgagggtc cagcactagg caaatgctat ttacgatctg 240
 caaaagctgt ttgaagagtc aaagccccc tgtgaacacg atttctggac cctgtaacag 300
 t 301

<210> 286
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 286
 taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaacttttgc 60
 tgtatattat ttttgcccta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
 atcaaaatgt gtcattgccag taagagatgt tatattcttt tctcatttct tccccacca 180
 aaaataagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt 240
 gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttcccttg 300
 t 301

<210> 287
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 287
 tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
 cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatatg 120
 aatgattttg gttatgaacg cacagttagg gcagcagggc cagaatcctg accctctgcc 180
 ccgtgggttat ctctcccca gcttggtgct ctcattgtat cacagtattc cattttgttt 240
 gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaaatgc 300
 t 301

<210> 288
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 288
 gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
 agtcaatagg aagacaaatt ccagttccag ctcagtctgg gtatctgcaa agctgcaaaa 120
 gatctttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180
 aaaagcatct gcttttgatga tttaatttag ctcattctgg cactggaaga atccaaacag 240
 tctgccttaa ttttgatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
 a 301

<210> 289
 <211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 289

```
ggtacactgt ttccatgta tgtttctaca cattgctacc tcagtgtcc tggaaactta      60
gcttttgatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatctttg    120
ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa    180
cgttctataa atgaatgtgc tgaagcaaag tgcccatggt ggcggcgaan aagagaaaga    240
tgtgttttgt tttggactct ctgtggtccc ttccaatgct gtgggtttcc aaccagnnga    300
a
```

<210> 290

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 290

```
acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac      60
tgactgatct gttcatttct ctcacagctc ttaccccaa aagcttttcc accctaagtg    120
ttctgacctc cttttctaata cacagtaggg atagaggcag anccacctac aatgaacatg    180
gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctagcagtgc    240
tgccttgaac aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagtgag    300
a
```

<210> 291

<211> 301

<212> DNA

<213> Homo sapien

<400> 291

```
caggtaccaa tttcttctat cctagaaaca tttcatttta tgttgttgaa acataacaac      60
tatatcagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc    120
tttactcttt tgtttatagg tgaatcacia aatgtatttt tatgtattct gtagtccaat    180
agccatggct gtttacttca ttttaatttat ttagcataaa gacattatga aaaggcctaa    240
acatgagctt cacttcccca ctaactaatt agcatctggt atttcttaac cgtaatgcct    300
a
```

<210> 292

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 292

```

accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc      60
tgtattaaat aatttttaag tttaaaagat aaaataccat catttttaat gttggtattc      120
aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg      180
ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc      240
tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa      300
a                                                                                   301

```

```

<210> 293
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 293
ggtaccaagt gctggtgcc a gctgttacc tgttctcact gaaaagtctg gctaattgctc      60
ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcttagagc actgactgtt      120
aacacaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaaa gctgttctgt      180
gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg      240
ccgcgaccac gctaagccga attctgcaga tatccatcac actggcgggc gctcgagcat      300
g                                                                                   301

```

```

<210> 294
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 294
tgaccataaa caatatacac tagctatctt ttttaactgtc catcattagc accaatgaag      60
attcaataaaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag      120
tttaactata gtcacaganc ttaaattatc acattgtttt ctatgtctac tgaaaataag      180
ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc      240
cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt      300
t                                                                                   301

```

```

<210> 295
<211> 305
<212> DNA
<213> Homo sapien

```

```

<400> 295
gtactctttc tctccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta      60
cacatttcac tgtgatgtat atttgtgtgc aaaaaaaaaa gtgtctttgt ttaaaattac      120
ttggtttggt aatccatctt gctttttccc cattggaact agtcattaac ccattctctga      180
actggtagaa aaacrtctga agagctagtc tatcagcatc tgacagggtga attggatggt      240
tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttggtg      300
tctct                                                                                   305

```

```

<210> 296
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 296
aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct      60

```

```

cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg 120
attaataaga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180
tttgaaaaag tgattgaacg aaccacttag ctctcagatg atgaacactg ataagtcatt 240
tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg 300
c 301

```

<210> 297

<211> 300

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 297

```

actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta 60
aaggttttga aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga 120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt 180
tccatcattg ggagtgcact ggcacatccct caaaatttgt ctgggctggc ctgagtggtc 240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc aactggcgg 300

```

<210> 298

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 298

```

tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc cctcccgcg 60
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg 120
tgaagctctc agatcaatca cgggaagggc ctggcggttg tggccacctg gaaccaccct 180
gtcctgtctg tttacatttc actaycaggt tttctctggg cattacnatt tgttccccta 240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcagggtggct ctcagcgagg 300
t 301

```

<210> 299

<211> 301

<212> DNA

<213> Homo sapien

<400> 299

```

gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggctctctgc 60
tcactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct ccaggtagc 120
tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg 180
gagtttcgcc atgttggccg gctggtctca aactcctgac ctcaagcgac ctgcctgcct 240
cggcctccca aagtgtgga attataggca tgagtcaaca cgcccagcct aaagatattt 300
t 301

```

<210> 300

<211> 301

<212> DNA

<213> Homo sapien

<400> 300
 attcagtttt atttgcgtgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60
 tatgtcccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca 120
 gctgcattcc acaagggttct cagcctaata agtttcaacta cctgccagtc tcaaaactta 180
 gtaaagcaag accatgacat tccccacagg aaatcagagt ttgccccacc gtcttggttac 240
 tataaagcct gcctctaaca gtccttgctt cttcacacca atccccgagcg catcccccat 300
 g 301

<210> 301
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 301
 ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60
 agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggt 120
 gggaactcac aaagaccctc agagctgaga caccacaaac agtgggagct cacaaagacc 180
 ctgagagctg agacaccac aacagtggga gctcacaag accctcagag ctgagacacc 240
 cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300
 t 301

<210> 302
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 302
 aggtacacat ttagcttggt gtaaattgact cacaaaactg attttaaaat caagttaatg 60
 tgaattttga aaattactac ttaattcctaa ttcacaataa caatggcatt aaggtttgac 120
 ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg 180
 ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca 240
 caggatttga gatgctaagg cccagagat cgtttgatcc aacctctta ttttcagagg 300
 g 301

<210> 303
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 303
 aggtaccaac tgtggaaata ggtagaggat cattttttct ttccatatca actaagttgt 60
 atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac 120
 tggctaattg aactaccgct tgcattgtaa aaatgggtgt ttgtgaaatg atcataggcc 180
 agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc 240
 catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac 300
 c 301

<210> 304
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 304
 acatggatgt tattttgcag actgtcaacc tgaatttgta tttgcttgac attgcctaata 60
 tattagtttc agtttcagct taccacattt ttgtctgcaa catgcaraas agacagtgcc 120
 ctttttagtg tatcatatca ggaatcatct cacattggtt tgtgccatta ctgggtgcagt 180
 gactttcagc cacttggtga aggtggagtt ggccatatgt ctccactgca aaattactga 240

ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct 300
c 301

<210> 305
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 305
gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag 60
caggggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggag 120
taaaggagga gaaacagata caaaatctcc aactcagtat taaggatttc tcatgcctag 180
aatattggta gaaacaagaa tacattcata tggcaataaa ctaaccatgg tggaacaaaa 240
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag 300
a 301

<210> 306
<211> 8
<212> PRT
<213> Homo sapien

<400> 306
Val Leu Gly Trp Val Ala Glu Leu
1 5

<210> 307
<211> 637
<212> DNA
<213> Homo sapien

<400> 307
acagggtratg aagggaaagg gagaggatga ggaagccccc ctggggattt ggtttggtcc 60
ttgtgatcag gtggtctatg gggcttatcc ctacaaagaa gaatccagaa atagggggcac 120
attgaggaat gataacttgag cccaaagagc attcaatcat tgttttattt gccttmtttt 180
cacaccattg gtgagggagg gattaccacc ctggggttat gaagatgggt gaacacccca 240
cacatagcac cggagatatg agatcaacag tttcttagcc atagagattc acagcccaga 300
gcaggaggac gcttgcacac catgcaggat gacatggggg atgcgctcgg gattggtgtg 360
aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacgggtggg caaactctga 420
tttcctgtgg ggaatgtcat ggtcttgctt tactaagttt tgagactggc aggtagtga 480
actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca 540
ggtgggagcc tttcccagtg ggtgtgggac atatctggca agattttgtg gcactcctgg 600
ttacagatac tggggcagca aataaaactg aatcttg 637

<210> 308
<211> 647
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(647)
<223> n = A,T,C or G

<400> 308

acgattttca	ttatcatgta	aatcgggtoa	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccaa	ggttctatac	aggatataaa	120
ggngcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccacccctct	gacccttttg	aactcctctg	acccttttaga	acaagcctac	ctaatatctg	240
ctagagaaaa	gaccaacaac	ggcctcaaa	gatctcttac	catgaaggtc	tcagctaatt	300
cttggctaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
cattttgtgt	gtggataaag	tcaggatgcc	cagggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taaccatagg	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgtatcaatt	gccatgaaga	cttgagggac	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggaac	aatgcagcag	cagaatcaat	ggaacaaca	gaatgattgc	600
aatgtccttt	tttttctcct	gcttctgact	tgataaaagg	ggaccgt		647

<210> 309

<211> 460

<212> DNA

<213> Homo sapien

<400> 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaaatac	tcatcatttt	tggccagcag	ttgtttgatc	180
accaaacatc	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtcag	240
ggggaattta	ttcctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctaccag	300
ctggggtggg	ggagcgaacc	cgtcactagt	ggacatgcag	tggcagagct	cctggtaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcactcaaat	420
ttgtcttggt	tttgtctttc	ggtgtgtaag	attcttaagt			460

<210> 310

<211> 539

<212> DNA

<213> Homo sapien

<400> 310

acgggactta	tcaaataaag	ataggaaaag	aagaaaactc	aaatattata	ggcagaaatg	60
ctaaaggttt	taaaatatgt	caggattgga	agaaggcatg	gataaagaac	aaagttcagt	120
taggaaagag	aaacacagaa	ggaagagaca	caataaaagt	cattatgtat	tctgtgagaa	180
gtcagacagt	aagatttggt	ggaaatgggt	tggtttgttg	tatggtatgt	attttagcaa	240
taatctttat	ggcagagaaa	gctaaaatcc	tttagcttgc	gtgaatgatc	acttgctgaa	300
ttcctcaagg	taggcatgat	gaaggagggt	ttagaggaga	cacagacaca	atgaactgac	360
ctagatagaa	agccttagta	tactcagcta	ggaatagtga	ttctgagggc	acactgtgac	420
atgattatgt	cattacatgt	atggtagtga	tggggatgat	aggaaggaag	aacttatggc	480
atattttcac	ccccacaaaa	gtcagttaaa	tattgggaca	ctaaccatcc	aggtcaaga	539

<210> 311

<211> 526

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (526)

<223> n = A,T,C or G

<400> 311

caaatttgag	ccaatgacat	agaattttac	aatcaagaa	gcttattctg	gggccatttc	60
ttttgacgtt	ttctctaaac	tactaaagag	gcattaatga	tccataaatt	atattatcta	120
catttacagc	atttaaaatg	tgttcagcat	gaaatattag	ctacagggga	agctaaataa	180

attaacatg	gaataaagat	ttgtccttaa	atataatcta	caagaagact	ttgatatttg	240
tttttcacaa	gtgaagcatt	cttataaagt	gtcataacct	ttttggggaa	actatgggaa	300
aaaatgggga	aactctgaag	ggttttaagt	atcttacctg	aagctacaga	ctccataacc	360
tctctttaca	gggagctcct	gcagccccta	cagaaatgag	tggctgagat	tcttgattgc	420
acagcaagag	cttctcatct	aaaccctttc	cctttttagt	atctgtgtat	caagtataaa	480
agttctataa	actgtagtnt	acttatttta	atcccctaa	cacagt		526

<210> 312
 <211> 500
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(500)
 <223> n = A,T,C or G

<400> 312	
cctctctctc	cccaccccct gactctagag aactgggttt tctcccagta ctccagcaat 60
tcattttctga	aagcagttga gccactttat tccaaagtac actgcagatg ttcaaactct 120
ccattttctct	ttcccttcca cctgccagtt ttgctgactc tcaacttgtc atgagtgtaa 180
gcattaagga	cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg 240
gcttcttagg	aaaatatttt tcttccaaaa tcagtaggaa atctaaactt atcccctctt 300
tgcagatgtc	tagcagcttc agacatttgg ttaagaaccc atgggaaaaa aaaaaatcct 360
tgctaattgtg	gtttcctttg taaaccanga ttcttatttg nctggatatag aatatcagct 420
ctgaacgtgt	ggtaaagatt tttgtgtttg aatataggag aaatcagttt gctgaaaagt 480
tagtcttaat	tatctattgg 500

<210> 313
 <211> 718
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(718)
 <223> n = A,T,C or G

<400> 313	
ggagatttgt	gtggtttgca gccgagggag accaggaaga tctgcatggt gggaaggacc 60
tgatgataca	gaggtgagaa ataagaaagg ctgctgactt taccatctga ggccacacat 120
ctgctgaaat	ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa 180
gtagtgacat	gtttttgcac atttccagcc cttttaaata tccacacaca caggaagcac 240
aaaagggaagc	acagagatcc ctgggagaaa tgcccggccg ccatcttggg tcatcgatga 300
gcctcgccct	gtgcctgntc ccgcttgtga gggaaggaca ttagaaaatg aattgatgtg 360
ttccttaaag	gatggcagga aaacagatcc tgttgtggat atttatttga acgggattac 420
agatttgaaa	tgaagtcaca aagtgagcat taccaatgag aggaaaacag acgagaaaat 480
cttgatgggt	cacaagacat gcaacaaaca aaatggaata ctgtgatgac acgagcagcc 540
aactggggag	gagataccac ggggcagagg tcaggattct ggccctgctg cctaactgtg 600
cgttatacca	atcatttcta ttctaccct caaacaagct gtngaataac tgacttacgg 660
ttcttntggc	ccacattttc atnatccacc cntcntttt aannttantic caaantgt 718

<210> 314
 <211> 358
 <212> DNA
 <213> Homo sapien

<400> 314

gtttattttac	attacagaaa	aaacatcaag	acaatgtata	ctattttcaaa	tatatccata	60
cataatcaaa	tatagctgta	gtacatgttt	tcattgggtg	agattaccac	aaatgcaagg	120
caacatgtgt	agatctcttg	tcttattctt	ttgtctataa	tactgtattg	tgtagtccaa	180
gctctcggtg	gtccagccac	tgtgaaacat	gctcccttta	gattaacctc	gtggacgctc	240
ttgttgatt	gctgaactgt	agtgccctgt	attttgcttc	tgtctgtgaa	ttctgttgct	300
tctggggcat	ttccttgtga	tgcagaggac	caccacacag	atgacagcaa	tctgaatt	358

<210> 315

<211> 341

<212> DNA

<213> Homo sapien

<400> 315

taccacctcc	ccgctggcac	tgatgagccg	catcaccatg	gtcaccagca	ccatgaaggc	60
ataggtgatg	atgaggacat	ggaatgggcc	ccaaggatg	gtctgtccaa	agaagcgagt	120
gacccccatt	ctgaagatgt	ctggaacctc	taccagcagg	atgatgatag	ccccaatgac	180
agtcaccagc	tccccgacca	gccggatata	gtccttaggg	gtcatgtagg	cttctgaag	240
tagctttctgc	tgtaagaggg	tgttgccccg	ggggctcgtg	cggttattgg	tcctgggctt	300
gagggggcgg	tagatgcagc	acatggtgaa	gcagatgatg	t		341

<210> 316

<211> 151

<212> DNA

<213> Homo sapien

<400> 316

agactgggca	agactcttac	gccccacact	gcaatttggt	cttggtgccc	tatccattta	60
tgtgggcctt	tctcgagttt	ctgattataa	acaccactgg	agcgatgtgt	tgactggact	120
cattcagggg	gctctgggtg	caatattagt	t			151

<210> 317

<211> 151

<212> DNA

<213> Homo sapien

<400> 317

agaactagtg	gattcctaag	aaataacctga	aacatatatt	ggcattttatc	aatggctcaa	60
atcttcattt	atctctggcc	ttaaccttgg	ctcctgaggg	tgcggccagc	agatcccagg	120
ccagggctct	gttcttgcca	cacctgcttg	a			151

<210> 318

<211> 151

<212> DNA

<213> Homo sapien

<400> 318

actgggtggga	ggcgtgttt	agttggctgt	tttcagaggg	gtctttcgga	gggacctcct	60
gctgcaggct	ggagtgtctt	tattcctggc	gggagaccgc	acattccact	gctgaggctg	120
tgggggcggg	ttatcaggca	gtgataaaca	t			151

<210> 319

<211> 151

<212> DNA

<213> Homo sapien

<400> 319

aactagtggg	tccagagcta	taggtacagt	gtgatctcag	ctttgcaaac	acattttcta	60
catagatagt	actaggtatt	aatagatatg	ttaaagaaaga	aatcacacca	ttaataatgg	120

taagattggg tttatgtgat tttagtgggt a 151

<210> 320

<211> 150

<212> DNA

<213> Homo sapien

<400> 320

aactagtgga tccactagtc cagtgtggtg gaattccatt gtgttggggt tctagatcgc 60
gagcggtgc cctttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120
gagtgttcta cagcttacag taaataccat 150

<210> 321

<211> 151

<212> DNA

<213> Homo sapien

<400> 321

agcaactttg tttttcatcc aggttatatt aggcttagga tttcctctca cactgcagtt 60
taggggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg 120
tgcctctgag aaatcaaagt cttcatacac t 151

<210> 322

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 322

atccagcacc ttctctgtt tcttgcttc cttttcttc ttcttasatt ctggttgagg 60
tttgggcttg gtcagtttg caccagggtt ggagatggg acagtcttct ggcattcggc 120
attgtgcagg gctcgttca nacttcagt t 151

<210> 323

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 323

tgaggacttg tkttttttt ctttatattt aatcctctta ckttgtaa atattgccta 60
nagactcant tactaccag tttgtggtt twtgggagaa atgtaactgg acagttagct 120
gttcaatyaa aaagacactt ancccatgtg g 151

<210> 324

<211> 461

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)... (461)
 <223> n = A,T,C or G

<400> 324

acctgtgtgg	aatttcagct	ttcctcatgc	aaaaggattt	tgtatccccg	gcctacttga	60
agaagtgggc	agctaaagga	atccagggtg	ttgggtggac	tgtaataacc	tttgatgaaa	120
agagttacta	cgaatcccat	cttggttcca	gctatatcac	tgacagcatg	gtagaagact	180
gcgaacctca	cttctagact	ttcacgggtg	gacgaaacgg	gttcagaaac	tgccaggggc	240
ctcatacagg	gatatcaaaa	taccctttgt	gctacccagg	ccctggggaa	tcaggtgact	300
cacacaaatg	caatagtgtg	tactgcatc	tttacctgaa	ccaaagctaa	acccggtgtt	360
gccaccatgc	accatggcat	gccagagttc	aacactgttg	ctcttgaaaa	ttgggtctga	420
aaaaacgcac	aagagcccct	gccctgccct	agctgangca	c		461

<210> 325
 <211> 400
 <212> DNA
 <213> Homo sapien

<400> 325

acactgtttc	catgttatgt	ttctacacat	tgctacctca	gtgctcctgg	aaacttagct	60
tttgatgtct	ccaagtagtc	caccttcatt	taactctttg	aaactgtatc	atctttgcca	120
agtaagagtg	gtggcctatt	tcagctgctt	tgacaaaatg	actggctcct	gacttaacgt	180
tctataaatg	aatgtgctga	agcaaagtgc	ccatggtggc	ggcgaagaag	agaaagatgt	240
gtttttgttt	ggactctctg	tggtcccttc	caatgctgtg	ggtttccaac	caggggaagg	300
gtcccttttg	cattgccaag	tgccataacc	atgagcacta	cgctaccatg	gttctgcctc	360
ctggccaagc	aggctgggtt	gcaagaatga	aatgaatgat			400

<210> 326
 <211> 1215
 <212> DNA
 <213> Homo sapien

<400> 326

ggaggactgc	agccccgact	cgcagccctg	gcaggcggca	ctggtcatgg	aaaacgaatt	60
gttctgctcg	ggcgctcctg	tgcatccgca	gtgggtgctg	tcagccgcac	actgtttcca	120
gaactcctac	accatcgggc	tgggcctgca	cagtcttgag	gccgaccaag	agccagggag	180
ccagatggtg	gaggccagcc	tctccgtacg	gcacccagag	tacaacagac	ccttgctcgc	240
taacgacctc	atgctcatca	agttggacga	atccgtgtcc	gagtctgaca	ccatccggag	300
catcagcatt	gcttcgcagt	gccctaccgc	ggggaaactct	tgctcgtttt	ctggctgggg	360
tctgctggcg	aacggcagaa	tgctaccgt	gctgcagtgc	gtgaacgtgt	cgggtggtgtc	420
tgaggaggtc	tgcatgaagc	tctatgacct	gctgtaccac	cccagcatgt	tctgcgccgg	480
cggagggcaa	gaccagaagg	actcctgcaa	cgggtactct	ggggggcccc	tgatctgcaa	540
cgggtacttg	cagggccttg	tgtctttcgg	aaaagccccg	tgtggccaag	ttggcgtgcc	600
aggtgtctac	accaacctct	gcaaattcac	tgagtggata	gagaaaaccg	tccaggccag	660
ttactctggt	ggactgggaa	cccatgaaat	tgacccccaa	atacatcctg	cggaaggaat	720
tcaggaatat	ctgttcccag	cccctcctcc	ctcaggccca	ggagtccagg	ccccagcccc	780
ctcctccctc	aaaccaaggg	tacagatccc	cagccccctc	tccctcagac	ccaggagtcc	840
agacccccca	gccccctctc	cctcagaccc	aggagtccag	ccccctcctc	ctcagaccca	900
ggagtccaga	ccccccagcc	cctcctcctc	cagacccagg	ggtccaggcc	cccaacctct	960
cctccctcag	actcagaggt	ccaagcccc	aacctctct	tccccagacc	cagaggtcca	1020
ggtcccagcc	cctcctccct	cagacccagc	ggtccaatgc	cacctagact	ctccctgtac	1080
acagtgcctc	cttgtggcac	gttgacccaa	ccttaccagt	tggtttttca	ttttttgtcc	1140
ctttccctta	gatccagaaa	taaagtctaa	gagaagcgca	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa	aaaaa					1215

<210> 327
 <211> 220

<212> PRT

<213> Homo sapien

<400> 327

```

Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
 1          5          10          15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
          20          25          30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
          35          40          45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
          50          55          60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
          65          70          75          80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
          85          90          95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
          100          105          110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
          115          120          125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
          130          135          140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
          145          150          155          160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
          165          170          175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
          180          185          190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
          195          200          205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
          210          215          220

```

<210> 328

<211> 234

<212> DNA

<213> Homo sapien

<400> 328

```

cgctcgtctc tggtagctgc agccaaatca taaacggcga ggactgcagc ccgcactcgc      60
agccctggca ggcggcactg gtcattgaaa acgaattggt ctgctcgggc gtcctgggtc      120
atccgcagtg ggtgctgtca gccacacact gtttccagaa ctctacacc atcgggctgg      180
gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag gcca          234

```

<210> 329

<211> 77

<212> PRT

<213> Homo sapien

<400> 329

```

Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser
 1          5          10          15
Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu
          20          25          30
Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr
          35          40          45
His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
          50          55          60

```

Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala
65 70 75

<210> 330
<211> 70
<212> DNA
<213> Homo sapien

<400> 330
cccaacacaa tggcccgatc ccatccctga ctccgccctc aggatcgctc gtctctggta 60
gctgcagcca 70

<210> 331
<211> 22
<212> PRT
<213> Homo sapien

<400> 331
Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu
1 5 10 15
Val Ser Gly Ser Cys Ser
20

<210> 332
<211> 2507
<212> DNA
<213> Homo sapien

<400> 332
tgggtgccgct gcagccggca gagatgggtg agctcatgtt cccgctgttg ctccctcttc 60
tgcccttccct tctgtatatg gctgcgcccc aaatcaggaa aatgctgtcc agtgggggtgt 120
gtacatcaac tgttcagctt cctgggaaag tagttgtggt cacaggagct aatacaggta 180
tcgggaagga gacagccaaa gagctggctc agagaggagc tcgagtatat ttagcttgcc 240
gggatgtgga aaagggggaa ttggtggcca aagagatcca gaccacgaca gggaccagc 300
aggtgttggt gcggaaactg gacctgtctg atactaagtc tattcgagct ttgctaagg 360
gcttcttagc tgaggaaaag cacctccagc ttttgatcaa caatgcagga gtgatgatgt 420
gtccgtactc gaagacagca gatggctttg agatgcacat aggagtcaac cacttgggtc 480
acttctctct aacccatctg ctgctagaga aactaaagga atcagcccca tcaaggatag 540
taaattgtgtc ttccctcgca catcacctgg gaaggatcca ctcccataac ctgcaggggcg 600
agaaattcta caatgcaggc ctggcctact gtcacagcaa gctagccaac atcctcttca 660
cccaggaact ggcccggaga ctaaaaggct ctggcggttac gacgtattct gtacaccctg 720
gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg tgggtggcttt 780
tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac tgtgccttaa 840
cagaaggctt tgagattcta agtgggaatc atttcagtga ctgtcatgtg gcatgggtct 900
ctgcccagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt tgtgacctgc 960
tgggcctccc aatagactaa caggcagtcg cagttggacc caagagaaga ctgcagcaga 1020
ctacacagta cttcttgtca aaatgattct ccttcaaggt tttcaaaacc tttagcacia 1080
agagagcaaa accttccagc cttgcctgct tgggtgtccag ttaaaactca gtgtactgcc 1140
agattcgtct aaatgtctgt catgtccaga tttactttgc ttctgttact gccagagtta 1200
ctagagatat cataatagga taagaagacc ctcatatgac ctgcacagct cattttcctt 1260
ctgaaagaaa ctactaccta ggagaatcta agctatagca gggatgattt atgcaaattt 1320
gaactagctt ctttgttcac aattcagttc ctcccaacca accagtcttc acttcaagag 1380
ggccacactg caacctcagc ttaacatgaa taacaaagac tggctcagga gcagggttg 1440
cccaggcatg gtggatcacc ggaggtcagt agttcaagac cagcctggcc aacatgggtg 1500
aacccacct ctactaaaaa ttgtgtatat ctttgtgtgt ctctctgttt atgtgtgcca 1560
agggagtatt ttcacaaagt tcaaaacagc cacaataatc agagatggag caaaccagtg 1620
ccatccagtc tttatgcaaa tgaaatgctg caaagggag cagattctgt atatgttggt 1680
aactaccac caagagcaca tgggtagcag ggaagaagta aaaaaagaga aggagaatac 1740

tggaagataa	tgcacaaaat	gaaggggacta	gttaaggatt	aactagccct	ttaaggatta	1800
actagttaag	gattaatagc	aaaagayatt	aaatatgcta	acatagctat	ggaggaattg	1860
agggcaagca	cccaggactg	atgaggtctt	aacaaaaacc	agtgtggcaa	aaaaaaaaaa	1920
aaaaaaaaaa	aaaatccta	aaaacaaca	aacaaaaaa	acaattcttc	attcagaaaa	1980
attatcttag	ggactgatat	tggttaattat	ggtcaattta	ataatatttt	ggggcatttc	2040
cttacattgt	cttgacaaga	ttaaaatgtc	tgtgccaaaa	ttttgtattt	tatttgagaa	2100
cttcttatca	aaagtaatgc	tgccaaagga	agtctaagga	attagtagtg	ttcccatcac	2160
ttgtttggag	tgtgctattc	taaaagattt	tgatttcctg	gaatgacaat	tatatattta	2220
ctttggtggg	ggaaagagtt	ataggaccac	agtcttcact	tctgatactt	gtaaattaat	2280
cttttattgc	acttgttttg	accattaagc	tatatgttta	gaaatgggtca	ttttacggaa	2340
aaattagaaa	aattctgata	atagtgcaga	ataaatgaat	taatgtttta	cttaatttat	2400
attgaactgt	caatgacaaa	taaaaattct	ttttgattat	tttttgtttt	catttaccag	2460
aataaaaaacg	taagaattaa	aagtttgatt	acaaaaaaa	aaaaaaa		2507

<210> 333

<211> 3030

<212> DNA

<213> Homo sapien

<400> 333

gcaggcgact	tgcgagctgg	gagcgattta	aaacgctttg	gattcccccg	gcctgggtgg	60
ggagagcgag	ctgggtgccc	cctagattcc	ccgccccgc	acctcatgag	ccgacctcg	120
gtccatgga	gcccggcaat	tatgccacct	tggtatggagc	caaggatata	gaaggcttgc	180
tggtgagcggg	aggggggagg	aatctggctg	ccactcccc	tctgaccagc	caccagcgg	240
cgctacgct	gatgcctgct	gtcaactatg	cccccttggg	tctgccaggc	tcggcgggagc	300
cgccaaagca	atgccacca	tgccctgggg	tgccccaggg	gacgtcccca	gctcccgtgc	360
cttatggtta	ctttggaggg	gggtactact	cctgccgagt	gtcccggagc	tcgctgaaac	420
cctgtgcccc	ggcagccacc	ctggccgcgt	accccgcgga	gactccacag	gccgggggag	480
agtacccag	ycgccccact	gagtttgct	tctatccggg	atatccggga	acctaccagc	540
ctatggccag	ttacctggag	gtgtctgtgg	tgagactct	gggtgctcct	ggagaccgc	600
gacatgactc	cctgttgctt	gtggacagtt	accagtcttg	ggctctcgct	gggtggctgga	660
acagccagat	gtgttgccag	ggagaacaga	acccaccagg	tcccttttgg	aaggcagcat	720
ttgcagactc	cagcgggcag	caccctcctg	acgctgcgc	ctttcgtcgc	ggccgcaaga	780
aacycattcc	gtacagcaag	gggcagttgc	gggagctgga	gcgggagtat	gcggctaaca	840
agttcatcac	caaggacaag	aggcgcaaga	tctcggcagc	caccagcctc	tcggagcgcc	900
agattaccat	ctggtttcag	aaccgccggg	tcaaagagaa	gaaggttctc	gccaaaggta	960
agaacagcgc	taccctttaa	gagatctcct	tgctgggtg	ggaggagcga	aagtgggggt	1020
gtcctgggga	gaccaggaac	ctgccaaagg	caggctgggg	ccaaggactc	tgctgagagg	1080
ccccatagaga	caacacctt	cccaggccac	tggtgtgtg	actgttcctc	aggagcggcc	1140
tggtatccca	gtatgtgcag	ggagacggaa	ccccatgtga	cagccactc	caccaggggt	1200
cccaaagaac	ctggccaggt	cataatcatt	cactctgaca	gtggcaataa	tcacgataac	1260
cagtactagc	tgccatgatc	gttagcctca	tattttctat	ctagagctct	gtagagcact	1320
ttagaaccg	ctttcatgaa	ttgagctaat	tatgaataaa	tttgggaaggc	gatccctttg	1380
cagggaaagct	ttctctcaga	cccccttcca	ttacacctct	caccctggta	acagcaggaa	1440
gactgaggag	aggggaacgg	gcagattcgt	tgtgtggctg	tgatgtccgt	ttagcatttt	1500
tctcagctga	cagctgggta	ggtggacaat	tgtagaggct	gtctcttctt	ccctccttgt	1560
ccaccccata	gggtgtaccc	actggtcttg	gaagcaccca	tccttaatac	gatgattttt	1620
ctgtcgtgtg	aaaatgaagc	cagcaggctg	cccctagtca	gtccttctct	ccagagaaaa	1680
agagatttga	gaaagtgcct	gggttaattca	ccattaattt	cctcccccaa	actctctgag	1740
tcttccctta	atatttcttg	tggttctgac	caaagcaggt	catggtttgt	tgagcatttg	1800
ggatcccagt	gaagtagatg	tttgtagcct	tgcatactta	gcccttccca	ggcacaaacg	1860
gagtggcaga	gtggtgcca	cctgtttttc	ccagtccacg	tagacagatt	cacagtgcgg	1920
aattctggaa	gctggagaca	gacgggctct	ttgcagagcc	gggactctga	gagggacatg	1980
agggcctctg	cctctgtgtt	cattctctga	tgtcctgtac	ctgggctcag	tgccccgttg	2040
gactcatctc	ctggccgcgc	agcaaagcca	gcggttctgt	gctggctcct	cctgcacctt	2100
aggctggggg	tggggggcct	gccggcgcat	tctccacgat	tgagcgcaca	ggcctgaagt	2160
ctggacaacc	cgagaaccg	aagctccgag	cagcgggtcg	gtggcgagta	gtggggctcg	2220
tggcgagcag	ttggtggtgg	gccgcggcgg	ccactacctc	gaggacattt	ccctcccgga	2280

gccagctctc	ctagaaaccc	cgcggcggcc	gccgcagcca	agtgtttatg	gcccgcggtc	2340
gggtgggata	ctagccctgt	ctcctctcct	gggaaggagt	gaggggtggga	cgtgacttag	2400
acacctacaa	atctattttac	caaagaggag	cccgggactg	agggaaaagg	ccaaagagtg	2460
tgagtgcata	cggactgggg	gttcagggga	agaggacgag	gaggaggaag	atgaggtcga	2520
tttcttgatt	taaaaaatcg	tccaagcccc	gtggtccagc	ttaaggtcct	cggttacatg	2580
cgccgctcag	agcaggtcac	tttctgcctt	ccacgtcctc	cttcaaggaa	gccccatgtg	2640
ggtagctttc	aatatcgag	gttcttactc	ctctgcctct	ataagctcaa	acccaccaac	2700
gatcgggcaa	gtaaaccccc	tccctcgccg	acttcggaac	tggcgagagt	tcagcgagga	2760
tgggcctgtg	gggagggggc	aagatagatg	agggggagcg	gcatggtgcg	gggtgacccc	2820
ttggagagag	gaaaaaggcc	acaagagggg	ctgccaccgc	cactaacgga	gatggccctg	2880
gtagagacct	ttgggggtct	ggaacctctg	gactccccat	gctctaactc	ccacactctg	2940
ctatcagaaa	cttaaaacttg	aggattttct	ctgtttttca	ctcgcaataa	aytcagagca	3000
aacaaaaaaa	aaaaaaaaaa	aaaactcgag				3030

<210> 334
 <211> 2417
 <212> DNA
 <213> Homo sapien

<400> 334						
ggcgcccgct	ctagagctag	tgggatcccc	cgggctgcac	gaattcggca	cgagtgagtt	60
ggagttttac	ctgtattgtt	ttaatttcaa	caagcctgag	gactagccac	aaatgtaccc	120
agtttacaaa	tgaggaaaca	ggtgcaaaaa	ggttggtacc	tgtcaaagg	cgtatgtggc	180
agagccaaga	tttgagccca	gttatgtctg	atgaacttag	cctatgctct	ttaaacttct	240
gaatgctgac	cattgaggat	atctaaactt	agatcaattg	cattttccct	ccaagactat	300
ttacttatca	atacaataat	accaccttta	ccaatctatt	gttttgatac	gagactcaaa	360
tatgccagat	atatgtaaaa	gcaacctaca	agctctctaa	tcagtctcac	ctaaaagatt	420
cccgggatct	aataggctca	aagaaacttc	ttctagaaat	ataaaagaga	aaattggatt	480
atgcaaaaat	tcattattaa	tttttttcat	ccatccttta	attcagcaaa	catttatctg	540
ttgttgactt	tatgcagtat	ggccttttaa	ggattggggg	acaggtgaag	aacgggggtg	600
cagaatgcat	cctcctacta	atgaggtcag	tacacatttg	cattttaaaa	tgccctgtcc	660
agctgggcat	ggtggatcat	gcctgtaatc	tcaacattgg	aaggccaagg	caggaggatt	720
gcttcagccc	aggagttcaa	gaccagcctg	ggcaacatag	aaagaccca	tctctcaatc	780
aatcaatcaa	tgccctgtct	ttgaaaataa	aactctttaa	gaaaggttta	atgggcaggg	840
tgtggtagct	catgcctata	atacagcact	ttgggaggct	gaggcaggag	gatcacttta	900
gcccagaagt	tcaagaccag	cctgggcaac	aagtgcaccc	tcattctcaat	tttttaataa	960
aatgaataca	tacataagga	aagataaaaa	gaaaagttta	atgaaagaat	acagtataaa	1020
acaaatctct	tggacctaaa	agtatttttg	ttcaagccaa	atattgtgaa	tcacctctct	1080
gtgttgagga	tacagaatat	ctaagcccag	gaaactgagc	agaaagtcca	tgtactaact	1140
aatcaacccg	aggcaaggca	aaaatgagac	taactaatca	atccgaggca	aggggcaaat	1200
tagacggaac	ctgactctgg	tctattaagc	gacaactttc	cctctgttgt	atttttcttt	1260
tattcaatgt	aaaaggataa	aaactctcta	aaactaaaaa	caatgtttgt	caggagttac	1320
aaaccatgat	caactaatta	tggggaatca	taaaatatga	ctgtatgaga	tcttgatggg	1380
ttacaaagtg	taccactgtg	taatcacttt	aaacattaat	gaacttaaaa	atgaatttac	1440
ggagattgga	atgtttcttt	cctgttgtat	tagttggctc	aggctgccat	aacaaaatac	1500
cacagactgg	gaggcttaag	taacagaaat	tcatttctca	cagttctggg	ggctggaagt	1560
ccacgatcaa	ggtgcaggaa	aggcaggctt	cattctgagg	cccctctctt	ggctcacatg	1620
tggccaccct	cccactgcgt	gtcacatga	cctctttgtg	ctcctggaaa	gaggggtgtg	1680
gggacagagg	gaaagagaag	gagagggaac	tctctgggtg	ctcgtctttc	aaggacccta	1740
acctggggca	ctttggccca	ggcactgtgg	gggtgggggg	tgtggctgct	ctgctctgag	1800
tggccaagat	aaagcaacag	aaaaatgtcc	aaagtgtg	agcaaagaca	agccaccgaa	1860
cagggatctg	ctcatcagtg	tggggacctc	caagtgcgcc	accctggagg	caagccccca	1920
cagagcccat	gcaagggtgg	agcagcagaa	gaagggaatt	gtccctgtcc	tggcacatt	1980
cctcaccgac	ctggtgatgc	tggacactgc	gatgaatgg	aatgtggatg	agaatatgat	2040
ggactcccag	aaaaggagac	ccagctgctc	aggtggctgc	aaatcattac	agccttcac	2100
ctggggagga	actgggggcc	tggttctggg	tcagagagca	gcccagtgag	gggtgagagct	2160
acagcctgtc	ctgccagctg	gatccccagt	cccgggtcaac	cagtaatcaa	ggctgagcag	2220
atcaggcttc	cgggagctgg	tcttggggaag	ccagccctgg	gggtgagttg	ctcctgctgt	2280

ggtactgaga caatattgtc ataaattcaa tgcgcccttg tatccctttt tcttttttat	2340
ctgtctacat ctataatcac tatgcatact agtctttgtt agtgtttcta ttcmaactaa	2400
tagagatatg ttatact	2417

<210> 335

<211> 2984

<212> DNA

<213> Homo sapien

<400> 335

atccctcctt cccactctc ctttccagaa ggcacttggg gtcttatctg ttggactctg	60
aaaacacttc aggcgcctt ccaaggcttc cccaaacccc taagcagccg cagaagcgct	120
cccgagctgc cttctccac actcaggtga tgcagttgga gaggaagttc agccatcaga	180
agtacctgtc ggcccctgaa cgggccacc tggccaagaa cctcaagctc acggagaccc	240
aagtgaagat atggttccag aacagacgct ataagactaa gcgaaagcag ctctcctcgg	300
agctgggaga cttggagaag cactcctctt tgcggccct gaaagaggag gccttctccc	360
gggcctccct ggtctccgtg tataacagct atccttacta cccatacctg tactgcgtgg	420
gcagctggag cccagctttt tggtaatgcc agctcaggtg acaaccatta tgatcaaaaa	480
ctgccttccc caggggtgtc ctatgaaaag cacaaggggc caaggtcagg gagcaagagg	540
tgtgcacacc aaagctattg gagatttgcg tggaaatctc asattcttca ctggtgagac	600
aatgaaacaa cagagacagt gaaagtttta atacctaagt cattccccca gtgcatactg	660
taggtcattt tttttgcttc tggctacctg tttgaagggg agagagggaa aatcaagtgg	720
tattttccag cactttgtat gattttggat gagctgtaca cccaaggatt ctgttctgca	780
actccatcct cctgtgtcac tgaatatcaa ctctgaaaga gcaaaccctaa caggagaaaag	840
gacaaccagg atgaggatgt caccaactga attaaactta agtcagaag cctcctgttg	900
gccttggaa atggccaagg ctctctctgt ccctgtaaaa gagaggggca aatagagagt	960
ctccaagaga acgcctcat gctcagcaca tatttgcctg ggagggggag atgggtggga	1020
ggagatgaaa atatcagctt ttcttattcc tttttattcc ttttaaaatg gtatgccaac	1080
ttaagtattt acaggggtgg ccaaatagaa caagatgcac tcgctgtgat tttaagacaa	1140
gctgtataaa cagaactcca ctgcaagagg gggggccggg ccaggagaat ctccgcttgt	1200
ccaagacagg ggcctaagg gggctccac actgctgcta ggggctgttg cattttttta	1260
ttagttagaa gtggaaaggc ctcttctcaa ctttttccc ttgggctgga gaatttagaa	1320
tcagaagttt cctggagttt tcaggctatc atatatactg tatcctgaaa ggcaacataa	1380
ttcttcttcc cctcctttta aaattttgtg ttcttttttg cagcaattac tcaotaaagg	1440
gcttcatttt agtcagatt tttagtctgg ctgcacctaa cttatgcctc gcttatttag	1500
cccgagatct ggtctttttt tttttttttt tttttccgtc tccccaaagc tttatctgtc	1560
ttgacttttt aaaaaagttt gggggcagat tctgaattgg ctaaaagaca tgcattttta	1620
aaactagcaa ctcttatttc tttcctttta aaatacatag cattaaatcc caaatcctat	1680
ttaaagacct gacagcttga gaaggctact actgcattta taggaccttc tgggtggtct	1740
gctgttacgt ttgaagctg acaatccttg agaattcttg catgcagagg aggtagagg	1800
tatttgattt tcacagagga agaacacagc gcagaatgaa gggccaggct tactgagctg	1860
tccagtggag ggctcatggg tgggacatgg aaaagaaggc agcctaggcc ctggggagcc	1920
cagtccactg agcaagcaag ggactgagtg agccttttgc aggaaaaggc taagaaaaag	1980
gaaaaccatt ctaaaacaca acaagaaact gtccaaatgc tttgggaact gtgtttattg	2040
cctataatgg gtcccaaaa tgggtaacct agacttcaga gagaatgagc agagagcaaa	2100
ggagaaatct ggctgtcctt ccattttcat tctgttatct caggtgagct ggtagagggg	2160
agacattaga aaaaaatgaa acaacaaaac aattactaat gaggtacgct gaggcctggg	2220
agtctcttga ctccactact taattccgtt tagtgagaaa cctttcaatt ttcttttatt	2280
agaagggcca gcttactgtt ggtggcaaaa ttgccaatat aagttaatag aaagttggcc	2340
aatttcaccc cattttctgt ggtttgggct ccacattgca atgttcaatg ccacgtgctg	2400
ctgacaccga cgggagtact agccagcaca aaaggcaggg tagcctgaat tgctttctgc	2460
tctttacatt tcttttaaaa taagcattta gtgctcagtc cctactgagt actctttctc	2520
tcccctctc tgaatttaat tctttcaact tgcaatttgc aaggattaca catttctactg	2580
tgatgtatat tgtgttgcaa aaaaaaaaaa aagtgtcttt gtttaaaatt acttggtttg	2640
tgaatccatc ttgctttttc cccattggaa ctagtcatta acccatctct gaactggtag	2700
aaaaacatct gaagagctag tctatcagca tctgacaggt gaattggatg gttctcagaa	2760
ccatttcacc cagacagcct gtttctatcc tgtttaataa attagtttgg gttctctaca	2820
tgcataacaa accctgctcc aatctgtcac ataaaagtct gtgacttgaa gtttagtcag	2880

cacccccacc aaactttatt tttctatgtg ttttttgcaa catatgagtg ttttgaaaat 2940
 aaagtaccca tgtctttatt agaaaaaaaa aaaaaaaaaa aaaa 2984

<210> 336
 <211> 147
 <212> PRT
 <213> Homo sapien

<400> 336
 Pro Ser Phe Pro Thr Leu Leu Ser Arg Arg His Leu Gly Ser Tyr Leu
 1 5 10 15
 Leu Asp Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr
 20 25 30
 Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln
 35 40 45
 Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
 50 55 60
 Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
 65 70 75 80
 Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
 85 90 95
 Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
 100 105 110
 Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
 115 120 125
 Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro
 130 135 140
 Ala Phe Trp
 145

<210> 337
 <211> 9
 <212> PRT
 <213> Homo sapien

<400> 337
 Ala Leu Thr Gly Phe Thr Phe Ser Ala
 1 5

<210> 338
 <211> 9
 <212> PRT
 <213> Homo sapien

<400> 338
 Leu Leu Ala Asn Asp Leu Met Leu Ile
 1 5

<210> 339
 <211> 318
 <212> PRT
 <213> Homo sapien

<400> 339
 Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Pro Phe Leu
 1 5 10 15
 Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val

			20				25				30					
Cys	Thr	Ser	Thr	Val	Gln	Leu	Pro	Gly	Lys	Val	Val	Val	Val	Thr	Gly	
			35					40					45			
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Glu	Thr	Ala	Lys	Glu	Leu	Ala	Gln	Arg	
			50					55					60			
Gly	Ala	Arg	Val	Tyr	Leu	Ala	Cys	Arg	Asp	Val	Glu	Lys	Gly	Glu	Leu	
65								70					75			
Val	Ala	Lys	Glu	Ile	Gln	Thr	Thr	Thr	Gly	Asn	Gln	Gln	Val	Leu	Val	
											90			95		
Arg	Lys	Leu	Asp	Leu	Ser	Asp	Thr	Lys	Ser	Ile	Arg	Ala	Phe	Ala	Lys	
											105			110		
Gly	Phe	Leu	Ala	Glu	Glu	Lys	His	Leu	His	Val	Leu	Ile	Asn	Asn	Ala	
											120			125		
Gly	Val	Met	Met	Cys	Pro	Tyr	Ser	Lys	Thr	Ala	Asp	Gly	Phe	Glu	Met	
											135			140		
His	Ile	Gly	Val	Asn	His	Leu	Gly	His	Phe	Leu	Leu	Thr	His	Leu	Leu	
145												155			160	
Leu	Glu	Lys	Leu	Lys	Glu	Ser	Ala	Pro	Ser	Arg	Ile	Val	Asn	Val	Ser	
											170			175		
Ser	Leu	Ala	His	His	Leu	Gly	Arg	Ile	His	Phe	His	Asn	Leu	Gln	Gly	
											185			190		
Glu	Lys	Phe	Tyr	Asn	Ala	Gly	Leu	Ala	Tyr	Cys	His	Ser	Lys	Leu	Ala	
											200			205		
Asn	Ile	Leu	Phe	Thr	Gln	Glu	Leu	Ala	Arg	Arg	Leu	Lys	Gly	Ser	Gly	
											215			220		
Val	Thr	Thr	Tyr	Ser	Val	His	Pro	Gly	Thr	Val	Gln	Ser	Glu	Leu	Val	
225												235			240	
Arg	His	Ser	Ser	Phe	Met	Arg	Trp	Met	Trp	Trp	Leu	Phe	Ser	Phe	Phe	
											245			255		
Ile	Lys	Thr	Pro	Gln	Gln	Gly	Ala	Gln	Thr	Ser	Leu	His	Cys	Ala	Leu	
											260			270		
Thr	Glu	Gly	Leu	Glu	Ile	Leu	Ser	Gly	Asn	His	Phe	Ser	Asp	Cys	His	
											275			285		
Val	Ala	Trp	Val	Ser	Ala	Gln	Ala	Arg	Asn	Glu	Thr	Ile	Ala	Arg	Arg	
											290			300		
Leu	Trp	Asp	Val	Ser	Cys	Asp	Leu	Leu	Gly	Leu	Pro	Ile	Asp			
305												310			315	

```
<210> 340
<211> 483
<212> DNA
<213> Homo sapien
```

<400> 340						
gccgaggtct	gccttcacac	ggaggacacg	agactgcttc	ctcaagggct	cctgcctgcc	60
tggacactgg	tgggagggcg	tgtttagtgt	gctgttttca	gaggggtctt	tcgaggggac	120
ctcctgctgc	aggctggagt	gtctttattc	ctggcgggag	accgcacatt	ccactgctga	180
ggttggtggg	gcggtttatc	aggcagtgat	aaacataaga	tgtcatttcc	ttgactccgg	240
ccttcaattt	tctctttggc	tgacgacgga	gtccgtggtg	tcccgatgta	actgacccct	300
gctccaaacg	tgacatcact	gatgctcttc	tcggggggtg	tgatggcccg	cttggtcacg	360
tgtctaatct	cgccattcga	ctcttgctcc	aaactgtatg	aagacacctg	actgcacgtt	420
ttttctgggc	ttccagaatt	taaagtgaaa	ggcagcactc	ctaagctccg	actccgatgc	480
ctg						483

```
<210> 341
<211> 344
<212> DNA
<213> Homo sapien
```

<400> 341

ctgctgctga	gtcacagatt	tcattataaa	tagcctccct	aaggaaaata	caactgaatgc	60
tatttttact	aaccattcta	tttttataga	aatagctgag	agtttctaaa	ccaactctct	120
gctgccttac	aagtattaaa	tattttactt	ctttccataa	agagtagctc	aaaatatgca	180
attaatttaa	taattttcga	tgatgggttt	atctgcagta	atatgtatat	catctattag	240
aatttactta	atgaaaaact	gaagagaaca	aaatttgtaa	ccactagcac	ttaagtactc	300
ctgattctta	acattgtctt	taatgaccac	aagacaacca	acag		344

<210> 342

<211> 592

<212> DNA

<213> Homo sapien

<400> 342

acagcaaaaa	agaaactgag	aagcccaaty	tgctttcttg	ttaacatcca	cttatccaac	60
caatgtggaa	acttcttata	cttggttcca	ttatgaagtt	ggacaattgc	tgctatcaca	120
cctggcaggt	aaaccaatgc	caagagagtg	atggaaacca	ttggcaagac	tttggtgatg	180
accaggattg	gaattttata	aaaatattgt	tgatgggaag	ttgctaaagg	gtgaattact	240
tccctcagaa	gagtgtaaag	aaaagtcaga	gatgctataa	tagcagctat	tttaattggc	300
aagtgccact	gtggaaagag	ttcctgtgtg	tgctgaagtt	ctgaagggca	gtcaaattca	360
tcagcatggg	ctgtttggtg	caaatgcaaa	agcacaggtc	tttttagcat	gctgggtctt	420
cccgtgtcct	tatgcaaata	atcgtcttct	tctaaatttc	tcctaggctt	cattttccaa	480
agttcttctt	ggtttgtgat	gtcttttctg	ctttccatta	attctataaa	atagtatggc	540
ttcagccacc	cactcttcgc	cttagcttga	ccgtgagtct	cggctgccgc	tg	592

<210> 343

<211> 382

<212> DNA

<213> Homo sapien

<400> 343

ttcttgacct	cctctctctt	caagctcaaa	caccacctcc	cttattcagg	accggcactt	60
cttaatgttt	gtggctttct	ctccagcctc	tcttaggagg	ggtaatggtg	gagttggcat	120
cttgtaactc	tcctttctcc	tttcttcccc	tttctctgcc	cgcctttccc	atcctgctgt	180
agacttcttg	attgtcagtc	tgtgtcacat	ccagtgattg	ttttggtttc	tgttcccttt	240
ctgactgcc	aaggggctca	gaaccccagc	aatcccttcc	tttactacc	ttcttttttg	300
ggggtagttg	gaagggactg	aaattgtggg	gggaaggtag	gaggcacatc	aataaagagg	360
aaaccaccaa	gctgaaaaaa	aa				382

<210> 344

<211> 536

<212> DNA

<213> Homo sapien

<400> 344

ctgggcctga	agctgtaggg	taaatcagag	gcaggcttct	gagtgatgag	agtcctgaga	60
caataggcca	cataaacttg	gctggatgga	acctcacaat	aagggtggta	cctcttggtt	120
gtttaggggg	atgccaaagga	taaggccagc	tcagttatat	gaagagaagc	agaacaaaca	180
agtctttcag	agaaatggat	gcaatcagag	tgggatcccc	gtcacatcaa	ggtcacactc	240
caccttcattg	tgccctgaatg	gttgccagggt	cagaaaaaatc	caccctttac	gagtgcggct	300
tegacctat	atcccccgcc	cgcgtccctt	tctccataaa	attcttctta	gtagctatta	360
ccttcttatt	atttgatcta	gaaattgccc	tccttttacc	cctaccatga	gccctacaaa	420
caactaacct	gccactaata	gttatgtcat	ccctcttatt	aatcatcatc	ctagccctaa	480
gtctggccta	tgagtgacta	caaaaaggat	tagactgagc	cgaataacaa	aaaaaa	536

<210> 345

<211> 251

<212> DNA
<213> Homo sapien

<400> 345
acctttttgag gtctctctca ccacctccac agccaccgtc accgtgggat gtgctggatg 60
tgaatgaagc ccccatcttt gtgcctcctg aaaagagagt ggaagtgtcc gaggactttg 120
gcgtgggcca ggaaatcaca tctacactg cccaggagcc agacacattt atggaacaga 180
aaataacata tcggatttgg agagacactg ccaactggct ggagattaat ccggacactg 240
gtgccatttc c 251

<210> 346
<211> 282
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(282)
<223> n = A,T,C or G

<400> 346
cgcgtctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt 60
ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcagttaca aattctggga 120
agggagacta tacctggctc ttgccctaag tgagaggctt tccctccgc accaaaaaat 180
agaaaggctt tctatttcac tggcccagggt agggggaagg agagtaactt tgagtctgtg 240
ggtctcattt cccaagggtg cttcaatgct catnaaaacc aa 282

<210> 347
<211> 201
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(201)
<223> n = A,T,C or G

<400> 347
acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca 60
taaataatac ttttaaaaaa ntactancag cttttaccta ngctcctaaa tgcttgtaaa 120
tctgagactg actggacca cccagacca gggcaaagat acatgttacc atatcatctt 180
tataaagaat ttttttttgt c 201

<210> 348
<211> 251
<212> DNA
<213> Homo sapien

<400> 348
ctgttaatca caacatttgt gcatacttg tgccaagtga gaaaatgttc taaaatcaca 60
agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccctg ggcaggcaga 120
aggagacact cccagcatgg aggagggttt atcttttcat cctaggtcag gtctacaatg 180
ggggaagggt ttattataga actcccaaca gccacactca ctctgccac ccacccgatg 240
gccctgcctc c 251

<210> 349
<211> 251
<212> DNA

<213> Homo sapien

<400> 349

taaaaatcaa gccatttaat tgtatctttg aaggtaaaca atatatggga gctggatcac	60
aacccctgag gatgccagag ctatgggtcc agaacatggt gtggtattat caacagagtt	120
cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt	180
agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca	240
actcctgggt t	251

<210> 350

<211> 908

<212> DNA

<213> Homo sapien

<400> 350

ctggacactt tgcgagggt tttgctggct gctgctgctg cccgtcatgc tactcatcgt	60
agcccgcccg gtgaagctcg ctgctttccc tacctcctta agtgactgcc aaacgcccac	120
cggctggaat tgctctggtt atgatgacag agaaaatgat ctcttcctct gtgacaccaa	180
cacctgtaaa tttgatgggg aatgtttaag aattggagac actgtgactt gcgtctgtca	240
gttcaagtgc aacaatgact atgtgcctgt gtgtgggtcc aatggggaga gctaccagaa	300
tgagtgttac ctgcgacagg ctgcatgcaa acagcagagt gagatacttg tgggtgcaga	360
aggatcatgt gccacagtc atgaaggctc tggagaaact agtcaaaagg agacatccac	420
ctgtgatatt tgccagtttg gtgcagaatg tgacgaagat gccgaggatg tctggtgtgt	480
gtgtaatat gactgttctc aaaccaactt caatccccctc tgcgttctct atgggaaatc	540
ttatgataat gcatgccaaa tcaaagaagc atcgtgtcag aaacaggaga aaattgaagt	600
catgtctttg ggtcgatgtc aagataaac aactacaact actaagtctg aagatgggca	660
ttatgcaaga acagattatg cagagaatgc taacaaatta gaagaaagtg ccagagaaca	720
ccacatacct tgtccggaac attacaatgg cttctgcatg catgggaagt gtgagcattc	780
tatcaatatg caggagccat cttgcagggt tgatgctggt tatactggac aacactgtga	840
aaaaaggac tacagtgttc tatacgttgt tcccggctct gtacgatttc agtatgtctt	900
aatcgcag	908

<210> 351

<211> 472

<212> DNA

<213> Homo sapien

<400> 351

ccagttattt gcaagtggta agagcctatt taccataaat aatactaaga accaactcaa	60
gtcaaacctt aatgccattg ttattgtgaa ttaggattaa gtagtaattt tcaaaattca	120
cattaacttg attttaaaaat cagwtttgyg agtcatttac cacaagctaa atgtgtacac	180
tatgataaaa acaaccattg tattcctggt tttctaaaca gtcttaattt ctaacactgt	240
atatatacct cgacatcaat gaactttggt ttcttttact ccagtaataa agtaggcaca	300
gatctgtcca caacaaactt gccctctcat gccttgctc tcaccatgct ctgctccagg	360
tcagccccc tttggcctgt ttgttttgtc aaaaacctaa tctgcttctt gcttttcttg	420
gtaatatata tttagggaag atgttgcttt gccacacac gaagcaaagt aa	472

<210> 352

<211> 251

<212> DNA

<213> Homo sapien

<400> 352

ctcaaagcta atctctcggg aatcaaacca gaaaaggga aggatcttag gcatgggtgga	60
tgtggataag gccagggtcaa tggctgcaag catgcagaga aagaggtaca tcggagcgtg	120
caggctgcgt tccgtcctta cgatgaagac cacgatgcag ttcccaaaca ttgccactac	180
atacatggaa aggaggggga agccaacca gaaatgggtc ttctctaata ctgggatacc	240
aataagcaca a	251

<210> 353
<211> 436
<212> DNA
<213> Homo sapien

<400> 353
tttttttttt tttttttttt tttttttacaa caatgcagtc atttatttat tgagtatgtg 60
cacattatgg tattattact atactgatta tatttatcat gtgacttcta attaraaaat 120
gtatccaaaa gcaaaacagc agatatacaa aattaaagag acagaagata gacattaaca 180
gataaggcaa cttatacatt gacaatccaa atccaataca tttaaacatt tgggaaatga 240
gggggacaaa tggaagccar atcaaatttg tgtaaaacta ttcagtatgt ttcccttget 300
tcatgtctga raaggctctc ccttcaatgg ggatgacaaa ctccaaatgc cacacaaatg 360
ttaacagaat actagattca cactggaacg ggggtaaaga agaaattatt ttctataaaa 420
gggctcctaa tgtagt 436

<210> 354
<211> 854
<212> DNA
<213> Homo sapien

<400> 354
ccttttctag ttcaccagtt ttctgcaagg atgctgggta gggagtgtct gcaggaggag 60
caagtctgaa accaaatcta ggaaacatag gaaacgagcc aggcacaggg ctgggtgggcc 120
atcagggacc accctttggg ttgatatttt gcttaatctg catcttttga gtaagatcat 180
ctggcagtag aagctgttct ccagggtacat ttctctagct catgtacaaa aacatcctga 240
aggactttgt caggtgcctt gctaaaagcc agatgcgttc ggcacttcct tggctgagg 300
ttaattgcac acctacaggc actgggctca tgctttcaag tattttgtcc tcactttagg 360
gtgagtga aa gatccccatt ataggagcac ttgggagaga tcatataaaa gctgactcct 420
gagtacatgc agtaatgggg tagatgtgtg tgggtgtgtc tcattcctgc aagggtgctt 480
gttagggagt gtttccagga ggaacaagtc tgaaaccaat catgaaataa atggtagggtg 540
tgaactggaa aactaattca aaagagagat cgtgatatca gtgtggttga tacacattcg 600
caatatggaa ggctctaatt tgcccatatt tgaaataata attcagcttt ttgtaataca 660
aaataacaaa ggattgagaa tcatggtgtc taatgtataa aagaccaggg aaacataaat 720
atatcaactg cataaatgta aaatgcatgt gaccaagaa ggcccaaag tggcagacaa 780
cattgtaccc attttccctt ccaaaatgtg agcggcgggc ctgctgcttt caaggctgtc 840
acacgggatg tcag 854

<210> 355
<211> 676
<212> DNA
<213> Homo sapien

<400> 355
gaaattaagt atgagctaaa ttccctgtta aaacctctag gggtgacaga tctcttcaac 60
caggtcaaag ctgatcttct tggaatgtca ccaaccaagg gcctatatatt atcaaaagcc 120
atccacaagt catacctgga tgtcagcgaa gagggcacgg aggcagcagc agccactggg 180
gacagcatcg ctgtaaaaaag cctaccaatg agagctcagt tcaaggcgaa ccacccttc 240
ctgttcttta taaggcacac tcataccaac acgatcctat tctgtggcaa gcttgccct 300
ccctaattcag atgggggttga gtaaggctca aggttgacga tgaggtgcag agacaatcct 360
gtgactttcc cacggccaaa aagctgttca cacctcacgc acctctgtgc ctgagtttgc 420
tcatctgcaa aataggtcta ggatttcttc caaccatttc atgagttgtg aagctaaggc 480
tttgtaaatc atggaaaaag gtagacttat gcagaaagcc tttctggctt tcttatctgt 540
gggtgtctcat ttgagtgtg tccagtgaca tgatcaagtc aatgagtaaa attttaaggg 600
attagatttt ctgacttgt atgtatctgt gagatcttga ataagtgacc tgacatctct 660
gcttaaagaa aaccag 676

<210> 356

<211> 574
 <212> DNA
 <213> Homo sapien

<400> 356
 tttttttttt tttttcagga aaacattctc ttactttatt tgcattctcag caaagggttct 60
 catgtggcac ctgactggca tcaaaccaaa gttcgtaggc caacaaagat gggccactca 120
 caagcttccc attttagat ctacgtgcct atgagtatct gacacctgtt cctctcttca 180
 gtctcttagg gaggtctaaa tctgtctcag gtgtgctaag agtgccagcc caaggkggtc 240
 aaaagtccac aaaactgcag tctttgctgg gatagtaagc caagcagtgc ctggacagca 300
 gagttctttt cttgggcaac agataaccag acaggactct aatcgtgctc ttattcaaca 360
 ttcttctgtc tctgcctaga ctggaataaa aagccaatct ctctcgtggc acaggggaagg 420
 agatacaagc tcgtttacat gtgatagatc taacaaaggc atctaccgaa gtctgggtctg 480
 gatagacggc acagggagct cttaggtcag cgctgctggg tggaggacat tcttgagtcc 540
 agctttgcag cctttgtgca acagtacttt ccca 574

<210> 357
 <211> 393
 <212> DNA
 <213> Homo sapien

<400> 357
 tttttttttt tttttttttt tttttttttt tacagaatat aratgcttta tcaactgkact 60
 taatatggkg kcttggtcac tatacttaaa aatgcaccac tcataaatat ttaattcagc 120
 aagccacaac caaracttga ttttatcaac aaaaaccctt aaatataaac ggsaaaaaag 180
 atagatataa ttattccagt ttttttaaaa cttaaaarat attccattgc cgaattaara 240
 araarataag tggttatatg aaagaagggc attcaagcac actaaaraaa cctgaggkaa 300
 gcataatctg tacaaaatta aactgtcctt tttggcattt taacaaattt gcaacgktct 360
 tttttttctt tttctgtttt tttttttttt tac 393

<210> 358
 <211> 630
 <212> DNA
 <213> Homo sapien

<400> 358
 acagggtaaa caggaggatc cttgctctca cggagcttac attctagcag gaggacaata 60
 ttaatgttta taggaaaatg atgagtttat gacaaaggaa gtagatagtg ttttacaaga 120
 gcatagagta gggaagctaa tccagcacag ggaggtcaca gagacatccc taaggaagtg 180
 gagtttaaac tgagagaagc aagtgcctaa actgaaggat gtgttgaaga agaagggaga 240
 gtagaacaat ttgggcagag ggaaccttat agaccctaag gtgggaagggt tcaaagaact 300
 gaaagagagc tagaacagct ggagccgttc tccggtgtaa agaggagtca aagagataag 360
 attaaagatg tgaagattaa gatcttgggt gcattcaggg attggcactt ctacaagaaa 420
 tcaactgaagg gagtaatgtg acattacttt tcaacttcagg atggccattc taactccagg 480
 gggtagactg gactaggtaa gactggaggc aggtagacct cttctaaggc ctgcatagt 540
 gaaagacaaa aataagtggg gaaattcagg ggatagttaa aatcagtagg acttaatgag 600
 caagccagag gttcctccac aacaaccagt 630

<210> 359
 <211> 620
 <212> DNA
 <213> Homo sapien

<400> 359
 acagcattcc aaaatatata tctagagact aarrgtaa gctctatagt gaagaagtaa 60
 taattaaaaa atgctactaa tatagaaaat ttataatcag aaaaataaat attcagggag 120
 ctcaccagaa gaataaagtg ctctgccagt tattaaagga ttactgctgg tgaattaaat 180
 atggcattcc ccaagggaaa tagagagatt cttctggatt atgttcaata tttatttcac 240

aggattaact	gttttaggaa	cagatataaa	gcttcgccac	ggaagagatg	gacaaagcac	300
aaagacaaca	tgataacctta	ggaagcaaca	ctaccctttc	aggcataaaa	tttggagaaa	360
tgcaacatta	tgcttcatga	ataatatgta	gaaagaaggt	ctgatgaaaa	tgacatcctt	420
aatgtaagat	aactttataa	gaattctggg	tcaaataaaa	ttctttgaag	aaaacatcca	480
aatgtcattg	acttatcaaa	tactatcttg	gcatataacc	tatgaaggca	aaactaaaca	540
aacaaaaaagc	tcacaccaaa	caaaaccatc	aacttatttt	gtattctata	acatacgaga	600
ctgtaaagat	gtgacagtgt					620

<210> 360
 <211> 431
 <212> DNA
 <213> Homo sapien

<400> 360						
aaaaaaaaaa	agccagaaca	acatgtgata	gataaatatga	ttggctgcac	acttccagac	60
tgatgaatga	tgaacgtgat	ggactattgt	atggagcaca	tcttcagcaa	gagggggaaa	120
tactcatcat	ttttggccag	cagttgtttg	atcaccaaac	atcatgccag	aatactcagc	180
aaaccttctt	agctcttgag	aagtcaaagt	ccgggggaat	ttattcctgg	caattttaat	240
tggactcctt	atgtgagagc	agcggctacc	cagctggggg	ggtggagcga	acccgtcact	300
agtggacatg	cagtggcaga	gctcctggta	accacctaga	ggaatacaca	ggcacatgtg	360
tgatgccaaag	cgtgacacct	gtagcactca	aatttgtctt	gtttttgtct	ttcgggtgtg	420
agattcttag	t					431

<210> 361
 <211> 351
 <212> DNA
 <213> Homo sapien

<400> 361						
acactgattt	ccgatcaaaa	gaatcatcat	ctttaccttg	acttttcagg	gaattactga	60
actttcttct	cagaagatag	ggcacagcca	ttgccttggc	ctcacttgaa	gggtctgcat	120
ttgggtctct	tggtctcttg	ccaagtttcc	cagccactcg	agggagaaat	atcgggaggt	180
ttgacttctt	ccggggcttt	cccaggggct	tcaccgtgag	ccctgcggcc	ctcagggctg	240
caatcctgga	ttcaatgtct	gaaacctcgc	tctctgcctg	ctggacttct	gaggccgtca	300
ctgccactct	gtctctccagc	tctgacagct	cctcatctgt	ggtcctgttg	t	351

<210> 362
 <211> 463
 <212> DNA
 <213> Homo sapien

<400> 362						
acttcatcag	gccataatgg	gtgcctcccg	tgagaatcca	agcacctttg	gactgcgcga	60
tgtagatgag	ccggctgaag	atcttgcgca	tgcgcggtt	cagggcggaag	ttcttggcgc	120
ccccggtcac	agaaatgacc	aggttgggtg	ttttcaggtg	ccagtgtctg	gtcagcagct	180
cgtaaaggat	ttccgcgtcc	gtgtcgcagg	acagacgtat	atacttccct	ttcttcccca	240
gtgtctcaaa	ctgaatatcc	ccaaaggcgt	cggtaggaaa	ttccttgggtg	tgtttcttgt	300
agttccattt	ctcacttttg	ttgatctggg	tgcttccat	gtgctggctc	tgggcatagc	360
cacacttgca	cacattctcc	ctgataagca	cgatgggtgtg	gacaggaagg	aaggatttca	420
ttgagcctgc	ttatggaaac	tggtattgtt	agcttaaata	gac		463

<210> 363
 <211> 653
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1) ... (653)

<223> n = A, T, C or G

<400> 363

acccccgagt	ncctgngctgg	catactgnga	acgaccaacg	acacacccaa	gctcggcctc	60
ctcttgngga	ttctgggtga	catcttcatg	aatggcaacc	gtgccagwga	ggctgtcctc	120
tgggaggcac	tacgcaagat	gggactgcgt	cctgggggtga	gacatcctct	ccttggagat	180
ctaacgaaac	ttctcaccta	tgagttgtaa	agcagaaata	cctgnactac	agacgagtgc	240
ccaacagcaa	ccccccggaa	gtatgagttc	ctctrgggcc	tccgttccta	ccatgagasc	300
tagcaagatg	naagtgttga	gantcattgc	agaggttcag	aaaagagacc	cntcgtgact	360
ggctctgcaca	gttcatggag	gctgcagatg	aggccttgga	tgctctggat	gctgctgcag	420
ctgaggccga	agcccgggct	gaagcaagaa	cccgcattggg	aattggagat	gaggctgtgt	480
ntgggccctg	gagctgggat	gacattgagt	ttgagctgct	gacctgggat	gaggaaggag	540
atthttggaga	tccttggtcc	agaattccat	ttaccttctg	ggccagatac	caccagaatg	600
cccgtctcag	attccctcag	acctttgccg	gtccattat	tggtcstggt	ggt	653

<210> 364

<211> 401

<212> DNA

<213> Homo sapien

<400> 364

actagaggaa	agacgttaaa	ccactctact	accacttggtg	gaactctcaa	agggtaaatg	60
acaaagccaa	tgaatgactc	taaaaacaat	atthacattt	aatggtttgt	agacaataaa	120
aaaacaaggt	ggatagatct	agaattgtaa	catttttaaga	aaaccatagc	atthgacaga	180
tgagaaaagct	caattataga	tgcaaagtta	taactaaact	actatagtag	taaagaaata	240
catttcacac	ccttcatata	aattcactat	cttggttgta	ggcactccat	aaaatgtatc	300
acgtgcatag	taaatcttta	tatttgctat	ggcgttgcac	tagaggactt	ggactgcaac	360
aagtggatgc	gcggaatg	aaatcttctt	caatagccca	g		401

<210> 365

<211> 356

<212> DNA

<213> Homo sapien

<400> 365

ccagtgtcat	atthgggctt	aaaatttcaa	gaagggcact	tcaaattggct	ttgcatttgc	60
atgtttcagt	gctagagcgt	aggaatagac	cctggcgctcc	actgtgagat	gttcttcagc	120
taccagagca	tcaagtctct	gcagcaggct	attcttgggt	aaagaaatga	cttcacacaa	180
ctctccatcc	cctggctttg	gcttcggcct	tgcgttttctg	gcatcatctc	cgtaaatggt	240
gactgtcacg	atgtgtatag	tacagtttga	caagcctggg	tccatacaga	ccgctggaga	300
acattcggga	atgtccctt	tgtagccagt	ttcttcttctg	agctcccga	gagcag	356

<210> 366

<211> 1851

<212> DNA

<213> Homo sapien

<400> 366

tcatcaccat	tgccagcagc	ggcaccgtta	gtcaggtttt	ctgggaatcc	cacatgagta	60
cttccgtgtt	cttcattctt	cttcaatagc	cataaatctt	ctagctctgg	ctggctgttt	120
tcaacttctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttgttctgga	180
ttgctgtttt	cagaagagat	ttttaacatc	tgthtttctt	tgtagtcaga	aagtaactgg	240
caaattacat	gatgatgact	agaaacagca	tactctctgg	ccgtctttcc	agatcttgag	300
aagatacatc	aacattttgc	tcaagtagag	ggctgactat	acttgctgat	ccacaacata	360
cagcaagtat	gagagcagtt	cttccatata	tatccagcgc	atttaaatte	gcttttttct	420
tgattaaaaa	tttcaccact	tgctgttttt	gctcatgtat	accaagtagc	agtggtgtga	480
ggccatgctt	gttttttgat	tcgatatcag	caccgtataa	gagcagtgtc	ttggccatta	540

atttatcttc	attgtagaca	gcatagtgtg	gagtgggtatt	tccatactca	tctggaatat	600
ttggatcagt	gccatgttcc	agcaacatta	acgcacattc	atcttcctgg	cattgtacgg	660
cctttgtcag	agctgtcctc	tttttgttgt	caaggacatt	aagttgacat	cgtctgtcca	720
gcacgagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	gcagtcctct	780
tttgcttgtc	cctcttgttc	acatccgtgt	ccctgagcat	gacgatgaga	tcctttctgg	840
ggactttacc	ccaccaggca	gctctgtgga	gcttgtccag	atcttctcca	tggacgtggt	900
acctgggac	catgaaggcg	ctgtcatcgt	agtctcccca	agcgaccacg	ttgctcttgc	960
cgctcccttg	cagcagggga	agcagtggca	gcaccacttg	cacctcttgc	tcccaagcgt	1020
cttcacagag	gagtcgttgt	ggtctccaga	agtgccacg	ttgctcttgc	cgctccctct	1080
gtccatccag	ggaggaagaa	atgcaggaaa	tgaagatgc	atgcacgatg	gtatactcct	1140
cagccatcaa	acttctggac	agcaggtcac	ttccagcaag	gtggagaaaag	ctgtccaccc	1200
acagaggatg	agatccagaa	accacaatat	ccattcacaa	acaaacactt	ttcagccaga	1260
cacaggtact	gaaatcatgt	catctgcggc	aacatggtgg	aacctaccca	atcacacatc	1320
aagagatgaa	gacactgcag	tatatctgca	caacgtaata	ctcttcaccc	ataacaaaat	1380
aatataattt	tcctctggag	ccatatggat	gaactatgaa	ggaagaactc	cccgaagaag	1440
ccagtcgcag	agaagccaca	ctgaagctct	gtcctcagcc	atcagcgcca	cggacaggag	1500
tgtgtttctt	ccccagtgat	gcagcctcaa	gttatcccg	agctgccgca	gcacacgggtg	1560
gctcctgaga	aacaccccag	ctcttcgggt	ctaacacagg	caagtcaata	aatgtgataa	1620
tcacataaac	agaattaaaa	gcaaagtcac	ataagcatct	caacagacac	agaaaaggca	1680
tttgacaaaa	tccagcatcc	ttgtatttat	tgttgacagt	ctcagaggaa	atgcttctaa	1740
cttttcccca	tttagtatta	tgttggtgtg	gggcttgtca	taggtgggtt	ttattacttt	1800
aaggtatgtc	ccttctatgc	ctgttttgct	gaggggttta	attctcgtgc	c	1851

<210> 367

<211> 668

<212> DNA

<213> Homo sapien

<400> 367

cttgagcttc	caaataaygga	agactggccc	ttacacagst	caatgttaaa	atgaatgcac	60
ttcagtattt	tgaagataaa	atttgtatag	ctataccttg	ttttttgatt	cgatatcagc	120
accrtataag	agcagtgcct	tggccattaa	tttatctttc	attttagaca	gcrtagtgya	180
gagtgggtatt	tccatactca	tctggaatat	ttggatcagt	gccatgttcc	agcaacatta	240
acgcacattc	atcttcctgg	cattgtacgg	cctgtcagta	ttagacccaa	aaacaaatta	300
catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tatttaaagg	360
agaaaaactca	tttttatgcc	atgtattgaa	atcaaaccga	cctcatgctg	atatagtgtg	420
ctactgcata	cctttatcag	agctgtcctc	tttttgttgt	caaggacatt	aagttgacat	480
cgtctgtcca	gcaggagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	540
gcagtcctat	gagagtgaga	agacttttta	ggaaattgta	gtgcactagc	tacagccata	600
gcaatgatcc	atgtaactgc	aaacactgaa	tagcctgcta	ttactctgcc	ttcaaaaaaa	660
aaaaaaaa						668

<210> 368

<211> 1512

<212> DNA

<213> Homo sapien

<400> 368

gggtcgccca	ggggsgcgt	gggttttctt	cggttggttg	tgggttttcc	ctgggtgggg	60
tgggctgggc	trgaatcccc	tgctgggggt	ggcagggttt	ggctgggatt	gacttttytc	120
ttcaaacaga	ttggaaaccc	ggagttacct	gctagtttgt	gaaactgggt	ggtagacgcg	180
atctgttggc	tactactggc	ttctcctggc	tgttaaaagc	agatggtggt	tgaggttgat	240
tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tgggtgctgcc	gttgcttccc	ctgctgcagg	gagagcggca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtggtgccgc	420
cactgcttcc	cctgctgcag	ggggagtggt	aagagcaacg	tgggcgcttc	tggagaccac	480
gacgaytctg	ctatgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
ccctgctgca	gggggagcrg	caagagcaag	gtgggcgctt	ggggagacta	cgatgacagt	600

gccttcatgg	agcccaggta	ccacgtcgt	ggagaagatc	tggacaagct	ccacagagct	660
gcctgggtggg	gtaaagtccc	cagaaaggat	ctcatcgta	tgctcagga	cactgacgtg	720
aacaagaagg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgcca	tggaattca	780
gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
aggacagctc	tgayaaaggc	cgtacaatgc	caggaagatg	aatgtgcgtt	aatgttgctg	900
gaacatggca	ctgatccaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
rtctayaatg	aagataaatt	aatggccaaa	gcactgctct	tatayggtgc	tgatatcgaa	1020
tcaaaaaaca	aggtatagat	ctactaattt	tatcttcaaa	atactgaaat	gcattcattt	1080
taacattgac	gtgtgtaagg	gccagtcctc	cgtatttgga	agctcaagca	taacttgaat	1140
gaaaatattt	tgaaatgacc	taattatctm	agactttatt	ttaaattattg	ttattttcaa	1200
agaagcatta	gaggggtacag	tttttttttt	ttaaattgcac	ttctgggtaaa	tacttttggt	1260
gaaaacactg	aattttgtaa	aggttaatact	tactattttt	caatttttcc	ctcctaggat	1320
ttttttcccc	taatgaatgt	aagatggcaa	aatttgccct	gaaatagggt	ttacatgaaa	1380
actccaagaa	aagttaaaca	tgtttcagtg	aatagagatc	ctgctccttt	ggcaagttcc	1440
taaaaaacag	taatagatac	gaggtgatgc	gcctgtcagt	ggcaagggtt	aagatatttc	1500
tgatctcgtg	cc					1512

<210> 369

<211> 1853

<212> DNA

<213> Homo sapien

<400> 369

gggtcgccca	ggggsgcgt	gggctttcct	cgggtgggtg	tgggttttcc	ctgggtgggg	60
tgggtctggg	trgaatcccc	tgctgggggt	ggcaggtttt	ggctgggatt	gacttttytc	120
ttcaaacaga	ttggaaaccc	ggagttacct	gctagtgggt	gaaactgggt	ggtagacgcg	180
atctgttggc	tactactggc	ttctcctggc	tgtaaaaagc	agatgggtgg	tgaggttgat	240
tccatgccc	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tggtgctgcc	gttgcttccc	ctgctgcagg	gagagcggca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtgggtccgc	420
cactgcttcc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tgagagaccac	480
gacgayctg	ctatgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
ccctgctgca	gggggagcrg	caagagcaag	gtgggcgctt	ggggagacta	cgatgacagy	600
gccttcatgg	akcccaggta	ccacgtccrt	ggagaagatc	tggacaagct	ccacagagct	660
gcctgggtggg	gtaaagtccc	cagaaaggat	ctcatcgta	tgctcagga	cackgaygtg	720
aacaagargg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgcca	tggaattca	780
gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
aggacagctc	tgayaaaggc	cgtacaatgc	caggaagatg	aatgtgcgtt	aatgttgctg	900
gaacatggca	ctgatccaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
rtctayaatg	aagataaatt	aatggccaaa	gcactgctct	tatayggtgc	tgatatcgaa	1020
tcaaaaaaca	agcatggcct	cacaccactg	ytacttggtt	tacatgagca	aaaacagcaa	1080
gtsgtgaaat	ttttaatyaa	gaaaaaagcg	aatttaaaat	gcrctggata	gatatggaag	1140
ractgctctc	atacttgctg	tatgttggtg	atcagcaagt	atagtcagcc	ytctacttga	1200
gcaaaatrtt	gatgtatctt	ctcaagatct	ggaaagacgg	ccagagagta	tgctgtttct	1260
agtcacatc	atgtaatttg	ccagttactt	tctgactaca	aagaaaaaca	gatgttaaaa	1320
atctcttctg	aaaacagcaa	tccagaacaa	gacttaaagc	tgacatcaga	ggaagagtca	1380
caaaggctta	aaggaagtga	aaacagccag	ccagaggcat	ggaaactttt	aaatttaaac	1440
ttttggttta	atgttttttt	tttttgccct	aataatatta	gatagtccca	aatgaaatwa	1500
cctatgagac	taggctttga	gaatcaatag	attctttttt	taagaatctt	ttggctagga	1560
gcggtgtctc	acgcctgtaa	ttccagacc	ttgagaggct	gaggtgggca	gatcacgaga	1620
tcaggagatc	gagaccatcc	tggttaaacac	ggtgaaaccc	catctctact	aaaaatacaa	1680
aaacttagct	gggtgtggtg	gcgggtgcct	gtagtcccag	ctactcagga	rgctgaggca	1740
ggagaatggc	atgaaccggg	gaggtggagg	ttgcagtgg	ccgagatccg	ccactacact	1800
ccagcctggg	tgacagagca	agactctgtc	tcaaaaaaaaa	aaaaaaaaaaa	aaa	1853

<210> 370

<211> 2184

<212> DNA

<213> Homo sapien

<400> 370

ggcacgagaa	ttaaaaccc	cagcaaaaaca	ggcatagaag	ggacatacct	taaagtaata	60
aaaaccac	atgacaagcc	cacagccaac	ataatactaa	atggggaaaa	gttagaagca	120
tttcctctga	gaactgcaac	aataaaataca	aggatgctgg	atgtttgtcaa	atgccttttc	180
tgtgtctgtt	gagatgctta	tgtgactttg	cttttaattc	tgtttatgtg	attatcacat	240
ttattgactt	gcctgtgtta	gaccggaaga	gctggggtgt	ttctcaggag	ccaccgtgtg	300
ctgcggcagc	ttcgggataa	cttgaggctg	catcactggg	gaagaaacac	aytctgtcc	360
gtggcgctga	tggctgagga	cagagcttca	gtgtggcttc	tctgcgactg	gcttcttcgg	420
ggagttcttc	cttcatagtt	catccatag	gctccagagg	aaaattatat	tattttgtta	480
tggatgaaga	gtattacgtt	gtgcagatat	actgcagtgt	cttcatctct	tgatgtgtga	540
ttgggtaggt	tccaccatgt	tgccgcagat	gacatgattt	cagtacctgt	gtctggctga	600
aaagtgtttg	tttgtgaatg	gatattgtgg	tttctggatc	tcctcctctg	tgggtggaca	660
gctttctcca	ccttgctgga	agtacctgc	tgtccagaag	tttgatggct	gaggagtata	720
ccatcgtgca	tgcactcttc	atttctctga	tttcttctc	cctggatgga	cagggggagc	780
ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	gacgcttggg	840
agcaagaggt	gcaagtgggt	ctgccactgc	ttccctgtct	gcagggggagc	ggcaagagca	900
acgtggctgc	ttggggagac	tacgatgaca	gcgccttcat	ggatcccagg	taccacgtcc	960
atggagaaga	tctggacaag	ctccacagag	ctgcctgggt	gggtaaagtc	cccagaaagg	1020
atctcatcgt	catgctcagg	gacacggatg	tgaacaagag	ggacaagcaa	aagaggactg	1080
ctctacatct	ggcctctgcc	aatgggaatt	cagaagtagt	aaaactcgtg	ctggacagac	1140
gatgtcaact	taatgtcctt	gacaacaaaa	agaggacagc	tctgacaaaag	gccgtacaat	1200
gccaggaaga	tgaatgtgct	ttaatgttgc	tggaaacatgg	cactgatcca	aatattccag	1260
atgagtatgg	aaataccact	ctacactatg	ctgtctacaa	tgaagataaa	ttaatggcca	1320
aagcactgct	cttatacggt	gctgatatcg	aatcaaaaaa	caagcatggc	ctcacaccac	1380
tgctacttgg	tatacatgag	caaaaacagc	aagtgggtgaa	atttttaatc	aagaaaaaag	1440
cgaatttaaa	tgcgctggat	agatatggaa	gaactgctct	catacttgct	gtatgttgtg	1500
gatcagcaag	tatagtcagc	cctctacttg	agcaaaatgt	tgatgtatct	tctcaagatc	1560
tggaaagacg	gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	1620
ttctgactac	aaagaaaaac	agatgttaaa	aatctcttct	gaaaaacagca	atccagaaca	1680
agacttaaa	ctgacatcag	aggaagagtc	acaaaggctt	aaaggaagtg	aaaacagcca	1740
gccagaggca	tggaaaacttt	taaatttaaa	cttttggttt	aatgtttttt	ttttttgcct	1800
taataatatt	agatagtccc	aaatgaaatw	acctatgaga	ctaggctttg	agaatcaata	1860
gattcttttt	ttaagaatct	tttggctagg	agcgggtgtct	cacgcctgta	attccagcac	1920
cttgagaggg	tgaggtgggc	agatcacgag	atcaggagat	cgagaccatc	ctggctaaca	1980
cgggtgaaacc	ccatctctac	taaaaaataca	aaaacttagc	tgggtgtggg	ggcgggtgcc	2040
tgtagtccca	gctactcagg	argctgaggc	aggagaatgg	catgaaccgg	ggaggtggag	2100
gttgacgtga	gccgagatcc	gccactacac	tccagcctgg	gtgacagagc	aagactctgt	2160
ctcaaaaaaa	aaaaaaaaaa	aaaa				2184

<210> 371

<211> 1855

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (1855)

<223> n = A,T,C or G

<400> 371

tgcaacgcac	ggccagtgtc	tgtgccacgt	acactgacgc	cccctgagat	gtgcacgccg	60
cacgcgcacg	ttgcacgcgc	ggcagcggct	tggctggctt	gtaacggctt	gcacgcgcac	120
gccgcccccg	cataaccgtc	agactggcct	gtaacggctt	gcagggcgac	gccgcacgcg	180
cgtaacggct	tggctgcctt	gtaacggctt	gcacgtgcat	gctgcacgcg	cgtaaacggc	240
ttggctggca	tgtagccgct	tggcttggct	ttgcattytt	tgctkggctk	ggcgttgkty	300
tcttggattg	acgcttctct	cttggatkgc	cgtttctctc	ttggatkgac	gtttcytyty	360

tcgcgttcc	ttgctggact	tgacctttty	tctgctgggt	ttggcattcc	tttgggggtgg	420
gctgggtggt	ttctccgggg	gggktkgccc	ttcctgggggt	gggcgtgggk	cgcccccagg	480
gggcgtgggc	tttccccggg	tgggtgtggg	ttttcctggg	gtgggggtggg	ctgtgctggg	540
atccccctgc	tgggggttggc	agggtattgac	ttttttcttc	aaacagattg	gaaacccgga	600
gtaacntgct	agttggtgaa	actggttggg	agacgcgac	tgctggtact	actgtttctc	660
ctggctgtta	aaagcagatg	gtggctgagg	ttgattcaat	gccggctgct	tcttctgtga	720
agaagccatt	tgggtctcagg	agcaagatgg	gcaagtgggtg	cgccactgct	tccctgtgtg	780
caggggggagc	ggcaagagca	acgtggggcac	ttctggagac	cacaacgact	cctctgtgaa	840
gacgcttggg	agcaagaggt	gcaagtgggtg	ctgcccactg	cttccccctgc	tgcaggggag	900
cggcaagagc	aacgtggkcg	cttgggggaga	ctacgatgac	agcgccctca	tggakcccag	960
gtaccacgtc	crtggagaag	atctggacaa	gctccacaga	gctgcctggt	ggggtaaagt	1020
ccccagaaag	gatctcatcg	tcatgctcag	ggacactgay	gtgaacaaga	rggacaagca	1080
aaagaggact	gctctacatc	tggcctctgc	caatgggaat	tcagaagtag	taaaactcgt	1140
gctggacaga	cgatgtcaac	ttaatgtcct	tgacaacaaa	aagaggacag	ctctgacaaa	1200
ggccgtacaa	tgccaggaag	atgaatgtgc	gttaatgttg	ctggaacatg	gcactgatcc	1260
aaatattcca	gatgagtatg	gaaataccac	tctacatat	gctgtctaca	atgaagataa	1320
attaatggcc	aaagcactgc	tcttatacgg	tgctgatata	gaatcaaaaa	acaaggtata	1380
gatctactaa	ttttatcttc	aaaatactga	aatgcattca	ttttaacatt	gacgtgtgta	1440
agggccagtc	ttccgtatct	ggaagctcaa	gcataacttg	aatgaaaata	ttttgaaatg	1500
acctaattat	ctaagacttt	attttaaaata	ttgttatctt	caaagaagca	ttagagggtg	1560
cagttttttt	tttttaaatg	cacttctggg	aaatactttt	gttgaaaaca	ctgaatttgt	1620
aaaaggtaat	acttactatt	tttcaatttt	tccctcctag	gatttttttc	ccctaataag	1680
tgtaagatgg	caaaatttgc	cctgaaatag	gtttttacatg	aaaactccaa	gaaaagttaa	1740
acatgtttca	gtgaatagag	atcctgctcc	tttggaaggt	tcctaaaaaa	cagtaataga	1800
tacgagggtga	tgcgcctgtc	agtggcaagg	tttaagatat	ttctgatctc	gtgcc	1855

<210> 372

<211> 1059

<212> DNA

<213> Homo sapien

<400> 372

gcaacgtggg	cacttctgga	gaccacaacg	actcctctgt	gaagacgctt	gggagcaaga	60
gggtgcaagt	gtgctgccc	ctgcttcccc	tgctgcaggg	gagcggcaag	agcdaagtg	120
gcgcttgrrg	agactmcgat	gacagygcct	tcatggagcc	caggtaccac	gtccgtggag	180
aagatctgga	caagctccac	agagctgccc	tgggtggggt	aagtcgccag	aaaggatctc	240
atcgatcatg	tcagggacac	tgaygtgaac	aagarggaca	agcaaaagag	gactgctcta	300
catctggcct	ctgccaatgg	gaattcagaa	gtagtataaac	tctgtctgga	cagacgatgt	360
caacttaatg	tccttgacaa	caaaaagagg	acagctctga	yaaaggccgt	acaatgccag	420
gaagatgaat	gtgcgttaat	gttgctggaa	catggcactg	atccaaatat	tccagatgag	480
tatggaaata	ccactctrca	ctaygctrct	tayaatgaag	ataaattaat	ggccaaagca	540
ctgctcttat	ayggtgctga	tatcgaatca	aaaaacaagg	tatagatcta	ctaattttat	600
cttcaaaata	ctgaaatgca	ttcattttta	cattgacgtg	tgtaaggggc	agtcctccgt	660
atttggaagc	tcaagcataa	cttgaatgaa	aatattttga	aatgacctaa	ttatctaaga	720
ctttattttta	aatattgtta	ttttcaaaga	agcattagag	gggtacagttt	ttttttttta	780
aatgcacttc	tggtaaatac	ttttgttgaa	aacactgaat	ttgtaaaagg	taatacttac	840
tatttttcaa	tttttccctc	ctaggatttt	tttcccctaa	tgaatgtaag	atggcaaaat	900
ttgccctgaa	atagggtttta	catgaaaact	ccaagaaaag	ttaaacaatgt	ttcagtgaat	960
agagatcctg	ctcctttggc	aagtccctaa	aaaacagtaa	tagatcacgag	gtgatgcgcc	1020
tgatcagtggc	aaggttttaag	atattttctga	tctcgtgccc			1059

<210> 373

<211> 1155

<212> DNA

<213> Homo sapien

<400> 373

atgggtgggtg	aggttgattc	catgccgggt	gcctcttctg	tgaagaagcc	atttgggtctc	60
-------------	------------	------------	------------	------------	-------------	----

aggagcaaga	tgggcaagt	gtgctgccgt	tgcttcccct	gctgcagggg	gagcggcaag	120
agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atgggcaagt	ggtgccgcca	ctgcttcccc	tgctgcaggg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
tggtgctgcc	actgcttccc	ctgctgcagg	gggagcggca	agagcaaggt	gggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccaggtacc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctgggtgggt	aaagtcccca	gaaaggatct	catcgtcatg	480
ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
tctgccaatg	ggaattcaga	agtagtaaaa	ctcctgctgg	acagacgatg	tcaacttaat	600
gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcca	ggaagatgaa	660
tgtgcgttaa	tggtgctgga	acatggcact	gatccaaata	ttccagatga	gtatggaaat	720
accactctgc	actacgctat	ctataatgaa	gataaattaa	tggccaaagc	actgctctta	780
tatggtgctg	atatcgaaatc	aaaaaacaag	catggcctca	caccactgtt	acttgggtga	840
catgagcaaa	aacagcaagt	cgtgaaatct	ttaatcaaga	aaaaagcgaa	tttaaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgctgtat	gttgtggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgat	gtatcttctc	aagatctatc	tggaacagacg	1020
gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	ttctgactac	1080
aaagaaaaac	agatgctaaa	aatctcttct	gaaaacagca	atccagaaaa	tgtctcaaga	1140
accagaaata	aataa					1155

<210> 374
 <211> 2000
 <212> DNA
 <213> Homo sapien

<400> 374						
atggtggttg	aggttgattc	catgccggct	gcctcttctg	tgaagaagcc	atttgggtctc	60
aggagcaaga	tgggcaagt	gtgctgccgt	tgcttcccct	gctgcagggg	gagcggcaag	120
agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atgggcaagt	ggtgccgcca	ctgcttcccc	tgctgcaggg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
tggtgctgcc	actgcttccc	ctgctgcagg	gggagcggca	agagcaaggt	gggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccaggtacc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctgggtgggt	aaagtcccca	gaaaggatct	catcgtcatg	480
ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
tctgccaatg	ggaattcaga	agtagtaaaa	ctcctgctgg	acagacgatg	tcaacttaat	600
gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcca	ggaagatgaa	660
tgtgcgttaa	tggtgctgga	acatggcact	gatccaaata	ttccagatga	gtatggaaat	720
accactctgc	actacgctat	ctataatgaa	gataaattaa	tggccaaagc	actgctctta	780
tatggtgctg	atatcgaaatc	aaaaaacaag	catggcctca	caccactgtt	acttgggtga	840
catgagcaaa	aacagcaagt	cgtgaaatct	ttaatcaaga	aaaaagcgaa	tttaaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgctgtat	gttgtggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgat	gtatcttctc	aagatctatc	tggaacagacg	1020
gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	ttctgactac	1080
aaagaaaaac	agatgctaaa	aatctcttct	gaaaacagca	atccagaaca	agacttaaa	1140
ctgacatcag	aggaagagtc	acaaagggtc	aaaggcagtg	aaaatagcca	gccagagaaa	1200
atgtctcaag	aaccagaaat	aaataaggat	ggtgatagag	aggttgaaga	agaaatgaag	1260
aagcatgaaa	gtaataatgt	gggattacta	gaaaacctga	ctaattggtgt	cactgctggc	1320
aatggtgata	atggattaat	tcctcaaagg	aagagcagaa	cacctgaaaa	tcagcaattt	1380
cctgacaacg	aaagtgaaga	gtatcacaga	atttgcgaat	tagtttctga	ctacaaagaa	1440
aaacagatgc	caaaatactc	ttctgaaaac	agcaaccag	aaagactt	aaagctgaca	1500
tcagaggaag	agtcacaaa	gcttgagggc	agtgaaaatg	gccagccaga	gctagaaaat	1560
tttatggcta	tcgaagaaat	gaagaagcac	ggaagtactc	atgtcggatt	cccagaaaac	1620
ctgactaatg	gtgccactgc	tggaatgggt	gatgatggat	taattcctcc	aaggaagagc	1680
agaacacctg	aaagccagca	atttcctgac	actgagaatg	aagagtatca	cagtgcagaa	1740
caaaatgata	ctcagaagca	attttgtgaa	gaacagaaca	ctggaatatt	acacgatgag	1800
attctgattc	atgaagaaaa	gcagatagaa	gtggttgaaa	aaatgaattc	tgagctttct	1860
cttagttgta	agaaagaaaa	agacatcttg	catgaaaata	gtacgttgcg	ggaagaaatt	1920

gccatgctaa gactggagct agacacaatg aaacatcaga gccagctaaa aaaaaaaaaa 1980
 aaaaaaaaaa aaaaaaaaaa 2000

<210> 375
 <211> 2040
 <212> DNA
 <213> Homo sapien

<400> 375
 atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttggcttc 60
 aggagcaaga tgggcaagtg gtgctgccgt tgcttccctt gctgcaggga gagcggcaag 120
 agcaacgtgg gcacttctgg agaccacgac gactctgcta tgaagacact caggagcaag 180
 atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg 240
 ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag 300
 tgggtgctgcc actgcttccc ctgctgcagg gggagcggga agagcaaggt ggcgcttgg 360
 ggagactacg atgacagtgc cttcatggag ccaggtacc acgtccgtgg agaagatctg 420
 gacaagctcc acagagctgc ctggtggggt aaagtcccca gaaaggatct catcgtcatg 480
 ctgagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc 540
 tctgccaatg ggaattcaga agtagtaaaa ctctgctgg acagacgatg tcaacttaat 600
 gtccttgaca acaaaaagag gacagctctg ataaaggcgc tacaatgcca ggaagatgaa 660
 tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaaat 720
 accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta 780
 tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttgggtga 840
 catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca 900
 ctggatagat atggaaggac tgctctcata cttgtgtgat gttgtggatc agcaagtata 960
 gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg 1020
 gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac 1080
 aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaca agacttaag 1140
 ctgacatcag aggaagagtc acaaagggtc aaaggcagtg aaaatagcca gccagagaaa 1200
 atgtctcaag aaccagaaat aaataaggat ggtgatagag aggttgaaga agaaatgaag 1260
 aagcatgaaa gtaataatgt gggattacta gaaaacctga ctaatggtgt cactgctggc 1320
 aatggtgata atggattaat tcttcaaagg aagagcagaa cacctgaaaa tcagcaattt 1380
 cctgacaacg aaagtgaaga gtatcacaga atttgccaat tagtttctga ctacaaagaa 1440
 aaacagatgc caaataactc ttctgaaaac agcaaccag aacaagactt aaagtgcaca 1500
 tcagaggaag agtcacaaag gcttgagggc agtgaaaatg gccagccaga gaaaagatct 1560
 caagaaccag aaataaataa ggatggtgat agagagctag aaaattttat ggctatcgaa 1620
 gaaatgaaga agcacggaag tactcatgtc ggattcccag aaaacctgac taatggtgcc 1680
 actgctggca atggtgatga tggattaatt cctccaagga agagcagaac acctgaaagc 1740
 cagcaatttc ctgacactga gaatgaagag tatcacagtg acgaacaaaa tgatactcag 1800
 aagcaatttt gtgaagaaca gaacactgga atattacacg atgagattct gattcatgaa 1860
 gaaaagcaga tagaagtggg tgaaaaaatg aattctgagc tttctcttag ttgtaagaaa 1920
 gaaaaagaca tcttgcata aaatagtacg ttgcgggaag aaattgccat gctaagactg 1980
 gagctagaca caatgaaaca tcagagccag ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040

<210> 376
 <211> 329
 <212> PRT
 <213> Homo sapien

<400> 376
 Met Asp Ile Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe
 1 5 10 15
 Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
 20 25 30
 Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
 35 40 45
 Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
 50 55 60

```

Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65          70          75          80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
85          90          95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
100        105        110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
115        120        125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
130        135        140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145        150        155        160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
165        170        175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
180        185        190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
195        200        205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
210        215        220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225        230        235        240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
245        250        255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
260        265        270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
275        280        285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
290        295        300
Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
305        310        315        320
Ser Met Leu Phe Leu Val Ile Ile Met
325

```

```

<210> 377
<211> 148
<212> PRT
<213> Homo sapien

```

```

<220>
<221> VARIANT
<222> (1)...(148)
<223> Xaa = Any Amino Acid

```

```

<400> 377
Met Thr Xaa Pro Ser Trp Ser Pro Gly Thr Thr Ser Val Glu Lys Ile
1          5          10          15
Trp Thr Ser Ser Thr Glu Leu Pro Trp Trp Gly Lys Val Pro Arg Lys
20        25        30
Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
35        40        45
Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
50        55        60
Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
65        70        75        80
Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
85        90        95

```

Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
 115 120 125
 Lys Leu Met Ala Lys Ala Leu Leu Tyr Gly Ala Asp Ile Glu Ser
 130 135 140
 Lys Asn Lys Val
 145

<210> 378
 <211> 1719
 <212> PRT
 <213> Homo sapien

<400> 378
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val

			340					345				350			
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile
		355					360					365			
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Asn	Val	Ser	Arg	Thr	Arg	Asn	Lys
		370				375					380				
Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser
385					390					395				400	
Ser	Val	Lys	Lys	Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys
				405					410				415		
Cys	Arg	Cys	Phe	Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly
			420					425					430		
Thr	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys
		435					440					445			
Met	Gly	Lys	Trp	Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly
450						455					460				
Lys	Ser	Asn	Val	Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys
465					470					475				480	
Thr	Leu	Arg	Asn	Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys
				485					490				495		
Cys	Arg	Gly	Ser	Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp
			500				505						510		
Asp	Ser	Ala	Phe	Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu
		515					520					525			
Asp	Lys	Leu	His	Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp
		530				535					540				
Leu	Ile	Val	Met	Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln
545					550					555				560	
Lys	Arg	Thr	Ala	Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val
				565					570					575	
Val	Lys	Leu	Leu	Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn
			580					585					590		
Lys	Lys	Arg	Thr	Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu
		595					600					605			
Cys	Ala	Leu	Met	Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp
		610				615				620					
Glu	Tyr	Gly	Asn	Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys
625					630					635				640	
Leu	Met	Ala	Lys	Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys
				645					650				655		
Asn	Lys	His	Gly	Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys
			660				665					670			
Gln	Gln	Val	Val	Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala
			675				680					685			
Leu	Asp	Arg	Tyr	Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly
			690			695					700				
Ser	Ala	Ser	Ile	Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser
705					710					715				720	
Ser	Gln	Asp	Leu	Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser
				725					730					735	
His	His	His	Val	Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln
			740				745						750		
Met	Leu	Lys	Ile	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys
			755				760					765			
Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser
			770			775					780				
Gln	Pro	Glu	Lys	Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp
785					790					795				800	
Arg	Glu	Val	Glu	Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly

805										810					815						
Leu	Leu	Glu	Asn	Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn						
			820					825					830								
Gly	Leu	Ile	Pro	Gln	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Asn	Gln	Gln	Phe						
		835					840					845									
Pro	Asp	Asn	Glu	Ser	Glu	Glu	Tyr	His	Arg	Ile	Cys	Glu	Leu	Val	Ser						
	850					855					860										
Asp	Tyr	Lys	Glu	Lys	Gln	Met	Pro	Lys	Tyr	Ser	Ser	Glu	Asn	Ser	Asn						
865					870					875					880						
Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Leu						
			885					890						895							
Glu	Gly	Ser	Glu	Asn	Gly	Gln	Pro	Glu	Leu	Glu	Asn	Phe	Met	Ala	Ile						
			900					905					910								
Glu	Glu	Met	Lys	Lys	His	Gly	Ser	Thr	His	Val	Gly	Phe	Pro	Glu	Asn						
		915					920					925									
Leu	Thr	Asn	Gly	Ala	Thr	Ala	Gly	Asn	Gly	Asp	Asp	Gly	Leu	Ile	Pro						
	930					935				940											
Pro	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Ser	Gln	Gln	Phe	Pro	Asp	Thr	Glu						
945					950					955					960						
Asn	Glu	Glu	Tyr	His	Ser	Asp	Glu	Gln	Asn	Asp	Thr	Gln	Lys	Gln	Phe						
			965					970						975							
Cys	Glu	Glu	Gln	Asn	Thr	Gly	Ile	Leu	His	Asp	Glu	Ile	Leu	Ile	His						
			980					985					990								
Glu	Glu	Lys	Gln	Ile	Glu	Val	Val	Glu	Lys	Met	Asn	Ser	Glu	Leu	Ser						
		995					1000					1005									
Leu	Ser	Cys	Lys	Lys	Glu	Lys	Asp	Ile	Leu	His	Glu	Asn	Ser	Thr	Leu						
	1010					1015						1020									
Arg	Glu	Glu	Ile	Ala	Met	Leu	Arg	Leu	Glu	Leu	Asp	Thr	Met	Lys	His						
1025					1030					1035					1040						
Gln	Ser	Gln	Leu	Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met						
			1045						1050					1055							
Pro	Ala	Ala	Ser	Ser	Val	Lys	Lys	Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met						
			1060					1065					1070								
Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe	Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys						
	10																				

1265	1270	1275	1280
Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr			
1285	1290	1295	
Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp			
1300	1305	1310	
Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Gly Val			
1315	1320	1325	
His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala			
1330	1335	1340	
Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala			
1345	1350	1355	1360
Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn			
1365	1370	1375	
Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr			
1380	1385	1390	
Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr			
1395	1400	1405	
Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu			
1410	1415	1420	
Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly			
1425	1430	1435	1440
Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn			
1445	1450	1455	
Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser			
1460	1465	1470	
Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly			
1475	1480	1485	
Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu			
1490	1495	1500	
Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys			
1505	1510	1515	1520
Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser			
1525	1530	1535	
Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu			
1540	1545	1550	
Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser			
1555	1560	1565	
Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe			
1570	1575	1580	
Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe			
1585	1590	1595	1600
Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly			
1605	1610	1615	
Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro			
1620	1625	1630	
Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln			
1635	1640	1645	
Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile			
1650	1655	1660	
Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser			
1665	1670	1675	1680
Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn			
1685	1690	1695	
Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr			
1700	1705	1710	
Met Lys His Gln Ser Gln Leu			
1715			

<210> 379
 <211> 656
 <212> PRT
 <213> Homo sapien

<400> 379
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415

Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
 500 505 510
 Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys
 515 520 525
 Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly
 530 535 540
 Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser
 545 550 555 560
 Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
 565 570 575
 His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
 580 585 590
 Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
 595 600 605
 Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
 610 615 620
 Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
 625 630 635 640
 Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 645 650 655

<210> 380
 <211> 671
 <212> PRT
 <213> Homo sapien

<400> 380
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala

165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
 500 505 510
 Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp
 515 520 525
 Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys
 530 535 540
 His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala
 545 550 555 560
 Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg
 565 570 575
 Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His
 580 585 590
 Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
 595 600 605
 Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
 610 615 620
 Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys

625 630 635 640
 Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
 645 650 655
 Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 660 665 670

<210> 381
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 381
 ggagaagcgt ctgctggggc aggaaggggt ttccctgccc tctcacctgt ccctcaccaa 60
 ggtaacatgc ttcccctaag ggtatcccaa cccagggggc tcaccatgac ctctgagggg 120
 ccaatatccc aggagaagca ttggggagtt gggggcaggt gaaggaccca ggactcacac 180
 atcctggggc tccaaggcag aggagaggggt cctcaagaag gtcaggagga aaatccgtaa 240
 caagcagtca g 251

<210> 382
 <211> 3279
 <212> DNA
 <213> Homo sapiens

<400> 382
 cttcctgcag ccccatgct ggtgaggggc acgggcagga acagtggacc caacatggaa 60
 atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtgt 120
 cactgggagg ggacatcctg cagaaggtag gagttagcaa acacccgctg caggggaggg 180
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240
 gggcctggag ggcgtgagga ggagcgaggg ggctgcatgg ctggagttag ggatcagggg 300
 cagggcgcgga gatggcctca cacagggaaag agagggcccc tcctgcaggg cctcacctgg 360
 gccacaggag gacactgctt ttctcttagg gagttaggag ctgtggatgg tgctggacag 420
 aagaaggaca gggcctgggt cagggtgtcca gaggctgtcg ctggcttccc ttgggatca 480
 gactgcaggg agggagggcg gcagggttgt ggggggagtg acgatgagga tgacctgggg 540
 gtggctccag gccttggccc tgcttggggc ctacccagc ctccctcaca gtctctggc 600
 cctcagtctc tccctccac tccatcctcc atctggcctc agtgggtcat tctgactact 660
 gaactgacca taccagccc tgcccacggc cctccatggc tcccaatgc cctggagagg 720
 ggacatctag tcagagagta gtctgaaga ggtggcctct gcgatgtgcc tgtgggggca 780
 gcacctgca gatgggtccc gccctcatcc tgctgacctg tctgcaggga ctgtcctcct 840
 ggacctggcc ccttgtgtag gactgggacc ctgaagtccc ctcccatag gccaaagactg 900
 gaccttgtt cctctgttg gactccctgc ccatattctt gtgggagtgg gttctggaga 960
 catttctgtc tgttcttag agctgggaat tgctctcagt catctgcctg cgcggttctg 1020
 agagatggag ttgcctaggc agttattggg gccaatcttt ctactgtgt ctctcctcct 1080
 ttacccttag ggtgattctg ggggtccact tgtctgtaat ggtgtgcttc aaggtatcac 1140
 atcatggggc cctgagccat gtgcctgcc tgaaaagcct gctgtgtaca ccaaggtggg 1200
 gcattaccgg aagtggatca aggacacat cgcagccaac ccctgagtgc cctgtccca 1260
 cccctacctc tagtaaattt aagtccacct cacgttctgg catcacttgg ctttctgga 1320
 tgctggacac ctgaagcttg gaactcacct ggccgaagct cgagcctcct gagtccact 1380
 gacctgtgct ttctgggtgt gagtccaggg ctgctaggaa aaggaatggg cagacacagg 1440
 tgtatgcaa tgtttctgaa atgggtataa ttctgctcct tcttcggaa cactggctgt 1500
 ctctgaagac ttctcgctca gtttcagtga ggacacacac aaagacgtgg gtgacctgt 1560
 tgtttgtggg gtcagagat gggaggggtg gggcccaccc tggaagagtg gacagtga 1620
 caaggtggac actctctaca gatcactgag gataagctgg agccacaatg catgaggcac 1680
 acacacagca aggttgacgc tgtaaacata gcccacgctg tcctgggggc actgggaagc 1740
 ctagataagg ccgtgagcag aaagaagggg aggatcctcc tatgttgtt aaggagggac 1800
 tagggggaga aactgaaagc tgattaatta caggaggttt gttcaggtcc cccaaaccac 1860
 cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggt 1920
 ttattatggt ttgttacatt gataggatag atactgaaat cagcaaaca aacagatgta 1980
 tagattagag tgtggagaaa acagaggaaa acttgcagtt acgaagactg gcaacttggc 2040

```

tttactaagt tttcagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100
gtagctgac cagctgatag aggaactagc caggtggggg cctttccctt tggatggggg 2160
gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg tacaaagtaa ttccaactga ggaagctcac ctgaccccta 2280
gtgtccaggg tttttactgg ggggtctgtag gacgagtatg gagtacttga ataattgacc 2340
tgaagtcctc agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacagggg ttcatcacia atcccatctt tagcatgaag ggtctggcat 2460
ggcccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaatgtc 2520
atctcccagg agttattcaa ggggtgagccc tttacttggg atgtacaggc tttgagcagt 2580
gcagggctgc tgagtcaacc ttttattgta caggggatga gggaaagggg gaggatgagg 2640
aagccccctt ggggatttgg tttgggtctt tgatcagggt gtctatgggg ctatccctac 2700
aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattggtgag ggagggatta ccaccctggg 2820
gttatgaaga tggttgaaca cccacacat agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgtgc acaccatgca ggatgacatg 2940
ggggatgcgc tcgggattgg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
acaagacggt ggggcaaact ctgatttccg tgggggaatg tcatggtctt gctttactaa 3060
gttttgagac tggcaggtag tgaaactcat taggctgaga accttgtgga atgcagctga 3120
cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtttt 3279

```

<210> 383

<211> 154

<212> PRT

<213> Homo sapiens

<400> 383

```

Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
      5                                10                                15

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
      20                                25                                30

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
      35                                40                                45

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
      50                                55                                60

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
      65                                70                                75                                80

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
      85                                90                                95

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
      100                                105                                110

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
      115                                120                                125

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
      130                                135                                140

Ala Leu Glu Arg Gly His Leu Val Arg Glu
      145                                150

```


<210> 384
<211> 557
<212> DNA
<213> Homo sapiens

<400> 384
ggatcctcta gagcgccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60
aaagatgtgt tttgttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120
ggggaagggt cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggg 180
tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300
ctctgtagag agcagcattc ccagggaacct tggaaacagt tggcactgta aggtgcttgc 360
tccccaaagc acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420
ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480
tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttcc aaagtaaaaa 540
aaaaaaaaaa aaaaaaaa 557

<210> 385
<211> 337
<212> DNA
<213> Homo sapiens

<400> 385
ttcccagggt atgtgcgagg gaagacacat ttactatcct tgatgggggt gattccttta 60
gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120
tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
tatcagacag gtccagtttc cgcaccaaca cctgctgggt ccctgtcgtg gtctggatct 300
ctttggccac caattccccc ttttccacat cccggca 337

<210> 386
<211> 300
<212> DNA
<213> Homo sapiens

<400> 386
gggcccgtca ccggcccagg ccccgccctc cgagtccctc tccccgggtg cctgcccgca 60
gccgcgtcgg cccagagggt gggcgcgggg ctgcctctac cggctggcgg ctgtaactca 120
gcgaccttgg cccgaaggct ctagcaagga cccaccgacc ccagccgcgg cggcgggcgg 180
gcggactttg cccggtgtgt ggggcgggagc ggactgcgtg tccgcggacg ggcagcgaag 240
atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

<210> 387
<211> 537
<212> DNA
<213> Homo sapiens

<400> 387
gggcccagtc gggcaccaag ggactctttg caggcttccct tccctcgatc atcaaggctg 60
ccccctcctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
tgaaccagga ccggcttctg ggcggctgaa aggggcaagg aggcaaggac cccgtctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttccctc agcactgagg 240
gagggggctt gtttcccttc cctcccggcg acaagctcca gggcagggtg gtccctctgg 300
gcgggccagc acttcctcag acacaacttc ttctgtctgc tccagtcgtg gggatcatca 360
cttaccacc ccccaagttc aagaccaaact cttccagctg ccccttctgt gtttccctgt 420
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctcagcctgg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaa aaaaaaaa 537

<210> 388
<211> 520
<212> DNA
<213> Homo sapiens

<400> 388
aggataattt ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgaggttaaa ccagtttgca ttccccta atgtggaaaa taagaggact actcagcact 120
gtttgaagat tgcctcttct acagcttctg agaattgtgt tatttcactt gccaaagtga 180
ggacccccct cccaacatgc ccagccccac ccctaagcat ggctccctgt caccaggcaa 240
ccaggaaact gctacttgtg gacctcacca gagaccagga gggtttggtt agctcacagg 300
acttccccca cccagaaga ttagcatccc atactagact cataactcaac tcaactaggc 360
tcatactcaa ttgatggta ttagacaatt ccatttcttt ctggttatta taaacagaaa 420
atctttcctc ttctcattac cagtaaaggc tcttggtatc ttctgttgg aatgatttct 480
atgaacttgt cttattttaa tgggtgggtt ttttctggt 520

<210> 389
<211> 365
<212> DNA
<213> Homo sapiens

<400> 389
cggtgcccc gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagttaaggc tggatttcag atctgcctgg ttccagccgc agtgtgccct ctgctcccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggctccctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttctctct ccttcagcaa ggggcgttgc ccacattctc 300
tgaggggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365

<210> 390
<211> 221
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(221)
<223> n = A,T,C or G

<400> 390
tgctctccca tcttggtccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacggntt ctcatgggtg tggaacatct ctgcttgagg ttccaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

<210> 391
<211> 325
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(325)
<223> n = A,T,C or G

<400> 391

```

tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgcgcc cagcctggag ctgtcctcctg catctaccaa caatcagncg aggcgagcag 120
tagccagggc actgctgcca acagccagtc cnnataccat catgtnaccg ggtgngctct 180
naanttngat ntccanagcc ctacccatcn tagttctgct ctcccaccgg ntaccagccc 240
cactgcccag gaatcctaca gccagtaccc tgtcccgcag tctctaccta ccagtacgat 300
gagacctcgg gctactacta tgacc                                     325

```

<210> 392

<211> 277

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(277)

<223> n = A,T,C or G

<400> 392

```

atattgttta actccttcct ttatatcttt taacattttc atggngaaa gttcacatct 60
agtctcactt nggcagngn ctctacttg agtctcttcc ccggcctggn ccagtnghaa 120
antaccanga accgncatgn cttanaaen ncctggtttn tgggttnntc aatgactgca 180
tgcatgacac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240
ctgaggatac agcgccgcgt cctgtgttgc tggggaa                                     277

```

<210> 393

<211> 566

<212> DNA

<213> Homo sapiens

<400> 393

```

actagtccag tgtggtggaa ttgcgcggcg cgtcgacgga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacgtt 120
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
gagaaggctc agtttgtcca tcagcattat catgatatca ggactgggta cttggttaag 240
gaggggtcta ggagatctgt cccttttaga gacaccttac ttataatgaa gtatttggga 300
gggtggtttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
catttattaa tcatccctgc ctgtgtctat tattatatcc atatctctac gctggaaact 420
ttctgcctca atgtttactg tgcccttgtt ttgtctagtt tgtgttgttg aaaaaaaaaa 480
cattctctgc ctgagtttta attttgtcc aaagtatttt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaa aaaaaa                                     566

```

<210> 394

<211> 384

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

```

gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaatng gaccgggcca aggcctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggctttta ggagttttta gctgagtgct actgtagacc ccaaatacca 180
tcccaagatt atcgggagaa agggggcagt aattacccaa atccggttgg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggacccaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360

```

tgagcagatg gtttctgagg acgt

384

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

```
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgac 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcatg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcattct ctcactacag acctctgacc atgggacggg 360
gcagcctggg gagaccatcc aatcccaaat aaaatgcac 399
```

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

```
tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataaactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttagggga gggagtgagg gataaaaagaa gaaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt 403
```

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

```
actagtncag tgtgggtggaa ttcgcggccg cgtcgacctc naanccatct ctatagcaaa 60
tccatccccg ctccctgggtg gtnacagaat gactgacaaa 100
```

<210> 398

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 398
gcggcgcggt cgacagcagt tccgccagcg ctgcgccctg ggtgggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcactactgt gctcgcacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggcgcg ttcattangt ggctcaacaa ggagaagg 278

<210> 399

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(298)

<223> n = A,T,C or G

<400> 399
acggagggtg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
ggggtgceng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcattggc ctgggtcatgg accgcatggg ctccgtggag cgcattgggt 180
ccggcattga gcgcattggc ccgctggggc tcgaccacat ggcctccanc attgancgca 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcatggg 298

<210> 400

<211> 548

<212> DNA

<213> Homo sapiens

<400> 400
acatcaacta cttcctcatt ttaaggatg gcagttccct tcateccctt ttctgcctt 60
gtacatgtac atgtatgaaa ttctcttctc ttaccgaact ctctccacac atcacaagg 120
caaagaacca cagccttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt tttccacgt ttaaggggccc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta tttcatacag gctttgaggc caccatgtc acttatcccg 300
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttgggccca taattctggg cctttgttgt ttgttttaac tacttgggca tcccaggaag 420
ctttccagtg atctcctacc atgggcccc ctctgaggat caagcccctc ccaggccctg 480
tccccagccc ctctgcccc agcccacccg cttgccttgg tgctcagccc tccattggg 540
agcaggtt 548

<210> 401

<211> 355

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(355)

<223> n = A,T,C or G

<400> 401
actgtttcca tggtatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60
tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa tgtgctgaag caaagtggcc atgggtggcg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnggg ttccaacca ggggaagggt 300

cccttttgcgca ttgccaagtg ccataacccat gagcactact ctaccatggn tctgc 355

<210> 402

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(407)

<223> n = A,T,C or G

<400> 402

```
atgggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
tctcacatgc ggtggcatat ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
aaatggaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180
gaataaagat aaaaaagaga aggacattac aaaggtggtc ctgacctttg ataaatctca 240
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300
ttgtggagct tctccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360
gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407
```

<210> 403

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 403

```
cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaattc aggcacccaa 60
tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
tagagaacaa gacctactca gtcatgaaca aaaaggcaga caccaacatg gatctcatgg 180
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240
tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catgttgaaa 300
gga 303
```

<210> 404

<211> 225

<212> DNA

<213> Homo sapiens

<400> 404

```
aagtgtgaact tttaaaaatt tagtggattt tgaaaattct tagaggaaaag taaaggaaaa 60
attgttaatg cactcattta cctttacatg gtgaaagttc tctcttgatc ctacaaacag 120
acattttcca ctcgtgtttc catagtgtgt aagtgtatca gatgtgttgg gcatgtgaat 180
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225
```

<210> 405

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(334)

<223> n = A,T,C or G

<400> 405

```
gagctgttat actgtgagtt ctactaggaa atcatcaa atctgagggtg tctggaggac 60
ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtcct tctccttact 120
tcatccccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180
ttccagtgct ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtg 240
ctggtgcggt tgtgcctcca gcttctgtc agtgcttcat ggacagtgtc cagcccatgt 300
cactctccac tctctcanng tggatccca cctt 334
```

<210> 406

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(216)

<223> n = A,T,C or G

<400> 406

```
tttcatacct aatgaggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aattttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant 216
```

<210> 407

<211> 413

<212> DNA

<213> Homo sapiens

<400> 407

```
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcattgc cttgactcat 60
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
gtacaacatt gcacccagtg tcagattcta cacctggcca ctcaggaagc aagagttaat 180
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atggggccagg ttctgtagta aag 413
```

<210> 408

<211> 183

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(183)

<223> n = A,T,C or G

<400> 408

```
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tncttaacta gttaatcctt aaagggtan ntaatcctta actagtcctt ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tatttactcc ttctgggcta cccatgtact 180
ntt 183
```

<210> 409

<211> 250

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(250)
<223> n = A,T,C or G

<400> 409
cccacgcatg ataagctctt tatttctgta agtctctgcta ggaaatcatc aaatctgacg 60
gtgggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
gcttcccagt gccccagga cagcgtgggc tatgtttaca gcgntcctt gctggggggg 240
ggccttatgc 250

<210> 410
<211> 306
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(306)
<223> n = A,T,C or G

<400> 410
ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tccatttgc aggatccgtc tgtgcacatg cctctgtaga gaggcagcatt 120
cccagggacc ttggaaacag ttggcactgt aagggtgctt ccccccaaga cacatcctaa 180
aagggtgttg aatgggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240
nactggttgg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
tcntgc 306

<210> 411
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

<400> 411
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tattaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa gngaggcaa a 261

<210> 412
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)

<223> n = A,T,C or G

<400> 412

ggttcaatggt acctgacatt tctacaacac cccactcacc gatgtattcg ttgcccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgcccagg aaatactacg 120
actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
ctgggagatt tctactgggta cattgaattc ccaaactacc cangcaatta cccagccaac 240
a 241

<210> 413

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(231)

<223> n = A,T,C or G

<400> 413

aactcttaca atccaagtga ctcactctgtg tgcttgaatc ctttccactg tctcatctcc 60
ctcatccaag tttctagtag cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
aagtttactc tctcatttg gaacctaaaa actctcttct tcttgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414

<211> 234

<212> DNA

<213> Homo sapiens

<400> 414

actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttcctttgg catgggatgg ggatgaagta aggagaggga 180
ctggaccccc tggaagctga ttcactatgg ggggaggtgt attgaagtcc tcca 234

<210> 415

<211> 217

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(217)

<223> n = A,T,C or G

<400> 415

gcataggatt aagactgagt atcttttcta cattctttta actttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggt tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc 217

<210> 416

<211> 213

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(213)
<223> n = A,T,C or G

<400> 416
atgcataatnt aaagganact gcctcgcttt tagaagacat ctggngctgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
cgaatgcaag gtggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag 213

<210> 417
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 417
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
gtgggaaagg ctttactctg agttcaaate ttcaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggtc 240
tcantcaaag ttcgtatctt caaatccatc ngaaggngcca cagtatanan aaacctttta 300
agt 303

<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 418
tttttggcgg tgggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcaactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180
gtatttttag tagagacagg gtttcaccat gttggccagg ctggtctcaa actcctnacc 240
tcagnggtca ggctggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
aaagtgctan gattacaggc cgtgagcc 328

<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

<400> 419
ctctctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatattg 60

```
acccttgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttctt ctctgtggct ccattcatag cacagttggt gcactgagge ttgtgcagge 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccggttctcc agccaccaac ctactcgtct cccgcaaagt gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389
```

<210> 420

<211> 408

<212> DNA

<213> Homo sapiens

<400> 420

```
gttcctccta actcctgcca gaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attccttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgtatg acaaacctgg caagcccc 408
```

<210> 421

<211> 352

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)... (352)

<223> n = A, T, C or G

<400> 421

```
gctcaaaaat ctttttactg atnggcattg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacagggtc tttttgggtc cttcttctcc accacnata acttgcagtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacagggt tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcattgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttctt gg 352
```

<210> 422

<211> 337

<212> DNA

<213> Homo sapiens

<400> 422

```
atgccaccat gctggcaatg cagcggggcg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgggcg cgtaactcct ggccaaggct agccgtgac 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcgggcgg cataagggt 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337
```

<210> 423

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
 <222> (1)...(310)
 <223> n = A,T,C or G

<400> 423
 gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
 aggagaatga ggctggcctt gggagccctg tgctactan aagcncatta gattatccat 120
 tcactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
 tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
 gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
 tccgagttaa 310

<210> 424
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(370)
 <223> n = A,T,C or G

<400> 424
 gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
 ggagaatgag gcctggcctt ggagccctgt gctactaga agcacattag attatccatt 120
 cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtcc 180
 ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
 ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
 cacgaagggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
 tccgtcgacg 370

<210> 425
 <211> 216
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(216)
 <223> n = A,T,C or G

<400> 425
 aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaata 60
 taacaacnca acatcaaggn aaananaaca ggaatggntg actntgcata aatnggccga 120
 anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccg 180
 gaggnnttca ggaccgctcg atgtnttntg aggagg 216

<210> 426
 <211> 596
 <212> DNA
 <213> Homo sapiens

<400> 426
 cttccagtga ggataaccct gttgccccgg gccgagggtc tccattagge totgattgat 60
 tggcagtcag tgatggaagg gtgttctgat cattccgact gccccaaggg tcgctggcca 120
 gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatggtga 180
 gctgtccttg tattttgatt aacctaattg ccttcccagc acgactcgga ttcagctgga 240
 gacatcacgg caacttttaa tgaaatgatt tgaagggccca ttaagaggca cttcccgtta 300

ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
gggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggg cacagcagat gtcattggtc tactgcctga 540
gtcccgtggt tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

<210> 427

<211> 107

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(107)

<223> n = A,T,C or G

<400> 427

gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncccag 60
cccgggagca gccttanaga gtcctgttt gactgcccgg ctcagng 107

<210> 428

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(38)

<223> n = A,T,C or G

<400> 428

gaacttcna anaangactt tattcactat tttacatt 38

<210> 429

<211> 544

<212> DNA

<213> Homo sapiens

<400> 429

ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttggatggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240
gccttcact tcagttacac ctcactcacc atcctctcct gttggttctg tgctgcttca 300
agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgtttctca tcaagcccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaacaa gtttagagaga tatgcatatc cagggatttt ttgccagggtg gtaggagaga 540
ttat 544

<210> 430

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(507)

<223> n = A,T,C or G

<400> 430

```
cttatacncaa tggggctccc aaacttggct gtgcagtgga aactccgggg gaattttgaa 60
gaacactgac acccatcttc caccctgaca ctctgattta attgggctgc agtgagaaca 120
gagcatcaat ttaaaaagct gccccagaatg ttntcctggg cagcggttgat atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgagggg gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcggtgt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagttaa tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctcctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa 507
```

<210> 431

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 431

```
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtccctgggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggcttttac tctgctgttt ct 392
```

<210> 432

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(387)

<223> n = A,T,C or G

<400> 432

```
ggtatcanta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcggn a gtccagccac tgngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngcctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtac aggaccggga 360
acaacgtata gaacactgga gtccttt 387
```

<210> 433

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(281)

<223> n = A, T, C or G

<400> 433

```

ttcaactagc anagaanact gcttcagggg gtgtaaaatg aaagggttcc acgcagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagnagg ntctctgtnt gccactggt 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

```

<210> 434

<211> 484

<212> DNA

<213> Homo sapiens

<400> 434

```

ttttaaaata agcatttagt gctcagtcct tactgagtac tctttctctc cctcctctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120
tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtaaa tccatcttgc 180
ttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaaccat ttcaccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaacc 360
tgctccaatc tgcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 484
ttaa

```

<210> 435

<211> 424

<212> DNA

<213> Homo sapiens

<400> 435

```

gcgcccgtca gagcaggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaacccc ctcctctgcc gacttcggaa ctggcgagag ttcagcgag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcatgggtc ggggtgacc 240
cttgagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaacctct ggactcccca tgccttaact cccacactct 360
gctatcagaa acttaaaact gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac

```

<210> 436

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(667)

<223> n = A, T, C or G

<400> 436

```

accttgggaa nactctcaca atataaaggg tegttagactt tactccaaat tccaaaaagg 60
tcttgccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattctc tgatttcaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactgt tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccaggtttg tcatagcact catcaaagtc cggtaacgt ctgtgcttcg aatataaacc 360

```

```
tggtcatgtt tataggactc attcaagaat tttctatata tctttcttat atactctcca 420
agttcataat gctgctccat gccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggtcagt gggaaaagggtg tcaatgggac ttcggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctcttggct agtacacttc ggtctagcca gaaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
tgttgag 667
```

<210> 437

<211> 693

<212> DNA

<213> Homo sapiens

<400> 437

```
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc aactaggac tctaccatac cgggttttgt 120
taaagctcag gttaggaggg tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtaactct ctattttcac cctcttggct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttgggggggac agccagcacc tttagctttc 420
atttgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540
tcctattttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcacatg tgctctcttg gctgaaaatg acc 693
```

<210> 438

<211> 360

<212> DNA

<213> Homo sapiens

<400> 438

```
ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac ctctgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgccca aagaatcttc aagaaggagg 180
actgcaagta tatctgggtg agaagaagga ccaaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360
```

<210> 439

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

```
gttctnnta actcctgcc a gaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgt gtttcggcat ggagaccgaa 180
gtcccattga cacttttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t 431
```


<210> 440
<211> 523
<212> DNA
<213> Homo sapiens

<400> 440
agagataaag cttaggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttacccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaaa tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tccctggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaac acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta 523

<210> 441
<211> 430
<212> DNA
<213> Homo sapiens

<400> 441
gttctctcta actcctgcc aaaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtt tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtgtg tgactttggt gtttcggcat ggagaccgaa 180
gtcccatgga cacttttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attccttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgctga cgcggccgcg 420
aatttagtag 430

<210> 442
<211> 362
<212> DNA
<213> Homo sapiens

<400> 442
ctaaggaatt agtagtggtc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcttgga tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatatt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362

<210> 443
<211> 624
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(624)
<223> n = A,T,C or G

<400> 443
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60

```

ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgagge ttaaataaac 360
taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtcacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaaact 600
ttgtccctat ctgctaaaca gatac 624

```

<210> 444

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(425)

<223> n = A,T,C or G

<400> 444

```

gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgggtg gtcagcaaat ccttgaatgc 180
tgcttaatgt gagagggttg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacacctg gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggtcgacg cggccgcgaa tttagtagta 420
gtaga 425

```

<210> 445

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 445

```

catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcattgtggc agattatttg atgtagtctt ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggtctctcc tcttgtattt tgaagcagtg 360
tggtgtctgg attgataaaa aaaaaaaaaa tgcacgcggc cgcaattta gtag 414

```

<210> 446

<211> 631

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(631)

<223> n = A,T,C or G

<400> 446

```
acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatgggt 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120
atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtggtgggc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaaacttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatggt tcacagtggc tggactaccg agagcttgga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccctg catttggtgt 540
aatctacacc aatgaaaaca tgtactacag ctatatttga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g                                     631
```

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 447

```
ccttgggaaa antntcacia tataaagggt cgtagacttt actccaaatt ccaaaaagggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccaggtttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcattgtt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagtggcc aaatcettgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggtca gtacacttcg gtcta                                     585
```

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 448

```
tgctcgtggg tcattctgan nncgaactg accntgccag ccctgccgan gggccnccat 60
ggctccctag tgccttgag agganggggc tag                                     93
```

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(706)

<223> n = A,T,C or G

<400> 449

```
ccaagttcat gctntgtgct ggacgctgga cagggggcaa aagcnnttgc tcgtgggtca 60
ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
cctggagagg aggtgtctag tcagagagta gtcctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggtcgggag cgteccattc gccattcagg ctgcgcaact 240
gttggaagg gcgatcgggt cgggcctctt cgctattacg ccagctggcg aaagggggat 300
gtgctgcaag gcgattaagt tgggtaacgc cagggttttc ccagtcncga cgttgtaaaa 360
cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcatgcacg 420
cgtacgtaag cttggatcct ctagagcggc cgcctactac tactaaattc gcggccgcgt 480
cgacgtggga tccnactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
aacaggttga acctgggagg tggaggttgc aatgagctga gatcaggccn ctgcncacca 660
gcatggatga cagagtgaaa ctccatctta aaaaaaaaaa aaaaaa 706
```

<210> 450

<211> 493

<212> DNA

<213> Homo sapiens

<400> 450

```
gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
acagttttta aaggtaaaac aacataaaaa gaaatatcct atagtggaaa taagagagtc 120
aaatgagggt gagaacttta caaagggtat ttacagacat gtcgccaata tcaactgcag 180
agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
caagtcaggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
agagacactg tcagagagtt aaaaagtggag ttctatccat gaggtgattc cacagtcttc 360
tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcggcc 480
gcgaatttag tag 493
```

<210> 451

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(501)

<223> n = A,T,C or G

<400> 451

```
gggcgcgtcc cattcgccat tcaggctgag caactgttgg gaagggcgat cgggtgcgggc 60
ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
gcggccgcct actactacta aattecgggc cgcgtcgacg tgggatacnc actgagagag 300
tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360
cgcncacagc actcacagct actcaggagg ctgagaacag gttgaacctg ggagggtggag 420
gttgcaatga gctgagatca ggccnctgcn ccccgacatg gatgacagag tgaaactcca 480
tcttaaaaaa aaaaaaaaaa a 501
```

<210> 452

<211> 51

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(51)
<223> n = A,T,C or G

<400> 452
agacggtttc accnttatac cnccttttag gatgggnntt ggggagcaag c 51

<210> 453
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(317)
<223> n = A,T,C or G

<400> 453
tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60
acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaacct 120
ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggtc tctacatgca 180
taacaaaccc tgcctcaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240
cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300
taccatgtc tttatta 317

<210> 454
<211> 231
<212> DNA
<213> Homo sapiens

<400> 454
ttcgaggtac aatcaactct cagagtgtag tttccttcta tagatgagtc agcatlaata 60
taagccacgc cagctcttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120
agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180
ccttctttt tcagtgttcc aaagctctc acaatttcac gaacaacagc t 231

<210> 455
<211> 231
<212> DNA
<213> Homo sapiens

<400> 455
taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60
cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120
gtttcaacgc attgatgact tctccaagga tcttcttttg gcatcgacca cattcagggg 180
caaagaattt ctcatagcac agtcacaat acagggtctc tttctcctct a 231

<210> 456
<211> 231
<212> DNA
<213> Homo sapiens

<400> 456
ttggcaggta cccttataaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcggt attattcttg gagaaacct gtctgtttac tgtaaccttt 120
tgcaactcaa ttcctttatc aggaataact acatagccac tatttataaa gccattggaa 180

cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaaag t 231

<210> 457

<211> 231

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(231)

<223> n = A,T,C or G

<400> 457

cgaggtagccc aggggtctga aaatctctnn ttantagtc gatagcaaaa ttgttcatca 60
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catacagttt 120
tatttgattt tattagcaat ctcttttcaga agacccttga gatcattaag ctttgatatcc 180
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458

<211> 231

<212> DNA

<213> Homo sapiens

<400> 458

agggtctggtt cccccactt ccactcccct ctactctctc taggactggg ctgggccaaag 60
agaagagggg tggttagggg agccgttgag acctgaagcc ccaccctcta ctttccttca 120
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
ggctcctgggt taggcatttt gggggggccag accccaggag aagaagattc t 231

<210> 459

<211> 231

<212> DNA

<213> Homo sapiens

<400> 459

ggtaccgagg ctcgctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60
ccttcgcgaa acctgtgggt gccaccagt cctaaccggga caggacagag agacagagca 120
gccttgcaat gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460

<211> 231

<212> DNA

<213> Homo sapiens

<400> 460

gcaggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaatt 120
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
gtggagcttg gtccagcctc cagtcacccc ctaccaggct taaggataga a 231

<210> 461

<211> 231

<212> DNA

<213> Homo sapiens

<400> 461

cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggaggggtc 60

gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcttg tgtgtcctgg 120
gtgggggttca gtgaggagtg ggaaattggt tcagcagaac caagccgttg ggtgaataag 180
agggggattc catggcactg atagagcctt atagtttcag agctgggaat t 231

<210> 462

<211> 231

<212> DNA

<213> Homo sapiens

<400> 462

aggtaaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
gggtcatgca agtataaaaa ttaaaaaaaa aagacttcat gccaatctc atatgatgtg 120
gaagaactgt tagagagacc aacagggtag tgggttagag atttccagag tcttacattt 180
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231

<210> 463

<211> 231

<212> DNA

<213> Homo sapiens

<400> 463

tactccagcc tgggtgacaga gcgagaccct atcaccgccc cccacccac caaaaaaaaa 60
actgagtaga cagggtgtcct ctgggcatgg taagtcttaa gtcccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cgggtgtccc atctgagtga gaaaaggcag 180
tggggagggtg gatcttccag tcgaagcggt atagaagccc gtgtgaaaag c 231

<210> 464

<211> 231

<212> DNA

<213> Homo sapiens

<400> 464

gtactctaag attttatcta agttgccttt tctgggtggg aaagttaaac cttagtgtact 60
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaataggg 120
cctgttccag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
gggtgccagcg caccagctag atgtctgtga acttctaggc cccattttcc c 231

<210> 465

<211> 231

<212> DNA

<213> Homo sapiens

<400> 465

catgttggtg tagctgtggt aatgctggct gcatctcaga cagggttaac ttcagctcct 60
gtggcaaatt agcaacaaat tctgacatca tatttatggt ttctgtatct ttgttgatga 120
aggatggcac aatttttctg tgtgttcata atatactcag attagttcag ctccatcaga 180
taaactggag acatgcagga cattagggta gtgtttagc tctggtaatg a 231

<210> 466

<211> 231

<212> DNA

<213> Homo sapiens

<400> 466

caggtaacctc tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60
ggccttcgaa cagaacttgc cacataccca ggtataatag tttctaacat ttgccaggga 120
cctgtgcaat caaatattgt ggagaattcc ctagctggag aagtcacaaa gactatagga 180
aataatggag accagtccca caagatgaca accagtcgtt gtgtgcggct g 231

<210> 467
 <211> 311
 <212> DNA
 <213> Homo sapiens

<400> 467
 gtacaccctg gcacagtcca atctgaactg gtctggcact catctttcat gagatggatg 60
 tgggtggcttt tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac 120
 tgtgccttaa cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180
 gcatgggtct ctgcccgaagc tcgtaatgag actatagcaa ggcggtctgtg ggacgtcagt 240
 tgtgacctgc tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga 300
 ctgcagcaga c 311

<210> 468
 <211> 3112
 <212> DNA
 <213> Homo sapiens

<400> 468
 catttgtgttg ggagaaaaac agagggggaga tttgtgtggc tgcagccgag ggagaccagg 60
 aagatctgca tgggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120
 tgggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180
 atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtgggtcaa 240
 cgaggacttg gaattgcatg gagctggagc tgaagtttag cccaattggt tactagttag 300
 gtgaatgtgg atgattggat gatcatttct catctctgag cctcagggtc cccatccata 360
 aaatgggata cacagtatga tctataaagt gggatatagt atgatctact tcaactgggt 420
 atttgaagga tgaattgaga taatttattt cagggtgcct gaacaatgcc cagattagta 480
 catttgtgttg aactgagaaa tggcataaca ccaaatttaa tatatgtcag atgttactat 540
 gattatcatt caatctcata gttttgtcat ggcccaattt atcctcactt gtgcctcaac 600
 aaattgaact gttaacaaaag gaatctctgg tcttgggtaa tggctgagca ccactgagca 660
 tttccattcc agttggcttc ttgggtttgc tagctgcac actagtcac ttaaataaat 720
 gaagttttta catttctcca gtgatttttt tatctcacct ttgaagatac tatgttatgt 780
 gattaaataa agaacttgag aagaacaggt ttcattaaac ataaaaatca ttagagcgca 840
 aattttctgg atgggcaata cttatgttca caggaaatgc tttaaaatat gcagaagata 900
 attaaatggc aatggacaaa gtgaaaaact tagacttttt tttttttttt ggaagtatct 960
 ggatgttctt tagtcaacta aaggagaact gaaaaatagc agtgagttcc acataatcca 1020
 acctgtgaga ttaaggctct ttgtggggaa ggacaaagat ctgtaaattt acagtttctt 1080
 tccaaagcca acgtcgaaat ttgaaacata tcaaagctct tcttcaagac aaataatcta 1140
 tagtacatct ttcttatggg atgcacttat gaaaaatggt ggctgtcaac atctagtcac 1200
 tttagctctc aaaatggttc attttaagag aaagtttttag aatctcata tttattcctgt 1260
 ggaaggacag cattgtggct tggactttat aaggtcttta ttcaactaaa taggtgagaa 1320
 ataagaaagg ctgctgactt taccatctga ggccacacat ctgctgaaat ggagataatt 1380
 aacatcacta gaaacagcaa gatgacaata taatgtctaa gtagtacat gtttttgcac 1440
 atttccagcc cctttaaata tccacacaca caggaagcac aaaaggaagc acagagatcc 1500
 ctgggagaaa tgcgccggcg ccatcttggg tcatcgatga gcctcgccct gtgcctggtc 1560
 ccgcttgtga ggggaaggaca ttagaaaatg aattgatgtg ttccttaaag gatgggcagg 1620
 aaaacagatc ctgttgtgga tatttatttg aacgggatta cagatttgaa atgaagtcac 1680
 aaagttagca ttaccaatga gagggaaaaca gacgagaaaa tcttgatggc ttcacaagac 1740
 atgcaacaaa caaaatggaa tactgtgatg acatgaggca gccaaagctgg ggaggagata 1800
 accacggggc agagggtcag gattctggcc ctgctgccta aactgtgcgt tcataacca 1860
 atcatttcat atttctaacc ctcaaaacaa agctgttgta atatctgac tctacgggtc 1920
 cttctgggcc caacattctc catatatcca gccacactca tttttaatat ttagtccca 1980
 gatctgtact gtgaccttc tacactgtag aataacatta ctcattttgt tcaaagacct 2040
 ttcgtgttgc tgcctaatat gtagctgact gtttttctta aggagtgttc tggcccaggg 2100
 gatctgtgaa caggctggga agcatctcaa gatctttcca gggttatact tactagcaca 2160
 cagcatgate attacggagt gaattatcta atcaacatca tctcagtggt ctttgcccat 2220
 actgaaattc atttccact tttgtgcca ttctcaagac ctcaaaatgt cattccatta 2280


```

atatcacagg attaactttt ttttttaacc tggaagaatt caatgttaca tgcagctatg 2340
ggaatttaat tacatatattt gttttccagt gcaaagatga ctaagtcctt tatccctccc 2400
ctttgtttga ttttttttcc agtataaagt taaaatgctt agccttgtae tgaggctgta 2460
tacagccaca gctctcctcc atccctccag ccttatctgt catcaccatc aaccctctcc 2520
atgcacctaa acaaaatcta acttgtaatt ccttgaacat gtcaggcata cattattcct 2580
tctgcctgag aagctcttcc ttgtctctta aatctagaat gatgtaaagt tttgaataag 2640
ttgactatct tacttcatgc aaagaaggga cacatatgag attcatcatc acatgagaca 2700
gcaaatacta aaagtgtaat ttgattataa gagtttagat aaatatatga aatgcaagag 2760
ccacagaggg aatgtttatg gggcacgttt gtaagcctgg gatgtgaagc aaaggcaggg 2820
aacctcatag tatcttatat aatatacttc atttctctat ctctatcaca atatccaaca 2880
agcttttcac agaattcatg cagtgc aaat ccccaaaggt aacctttatc catttcatgg 2940
tgagtgcgct ttagaatttt ggcaaatcat actggctact tatctcaact ttgagatgtg 3000
tttgtccttg tagttaattg aaagaaatag ggcactcttg tgagccactt taggggtcac 3060
tcttggcaat aaagaattta caaagagcaa aaaaaaaaaa aaaaaaaaaa aa 3112

```

<210> 469

<211> 2229

<212> DNA

<213> Homo sapiens

<400> 469

```

agctctttgt aaattcttta ttgccaggag tgaaccctaa agtggctcac aagagtgtcc 60
tatttctttc aattaactac aaggacaaac acatctcaaa gttgagataa gtgaccagta 120
tgatttgcca aaattctaaa gcgcactcac catgaaatgg ataaagggtta cctttgggga 180
tttgactgac atgaattctg tgaaaagctt gttggatatt gtgatagaga tagagaaatg 240
aagtatatta tataagatac tatgagggtc cctgcctttg ctccacatcc caggcttaca 300
aacgtgcccc ataaacattc cctctgtggc tcttgcattt catatattta tctaaactct 360
tataatcaaa tacactttta gtatttgctg tctcatgtga tgatgaatct catatgtgtc 420
ccttctttgc atgaagtaag atagtcaact tattcaaaac ttacatcat tctagattta 480
agagacaagg aagagcttct caggcagaag gaataatgta tgctgacat gttcaaggaa 540
ttacaagtta gattttgttt aggtgcatgg gaggggttga tggatgac agataaggct 600
ggagggatgg ggagaggctg tggctgtata cagcctcagt acaaggctaa gcattttaac 660
tttatactgg aaaaaaaatc aaacaaaggg gagggataaa ggacttagtc atctttgcac 720
tggaaaacaa aatatgtaat taaattccca tagctgcatg taacattgaa ttcttccagg 780
ttaaaaaaaa agttaatcct gtgatattaa tggaatgaca ttttgagggtc ttgagaatgg 840
gcacaaaagt gggaaatgaa tttcagtatg ggcaagaca ctgaggatga tgttgattag 900
ataattcact ccgtaatgat catgctgtgt gctagtaagt ataaccctgg aaagatcttg 960
agatgcttcc cagcctgttc acagatcccc tgggccagaa cactccttag gaaaaacagt 1020
cagctacata ttaggcagca acacgaaggg tctttgaaca aaatgagtaa tgttattcta 1080
cagtgtagaa aggtcacagt acagatctgg gaactaaata ttaaaaatga gtgtggctgg 1140
atatatggag aatgttgggc ccagaaggaa ccgtagagat cagatattac aacagctttg 1200
ttttgagggt tagaaatatg aaatgatttg gttatgaacg cacagttagg gcagcagggc 1260
cagaatcctg accctctgcc ccgtggttat ctctcccca gcttggctgc ctcatgtcat 1320
cacagtattc cattttgttt gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt 1380
tttctctca ttggaatgc tcactttgtg acttcatttc aaatctgtaa tcccgttcaa 1440
ataaatatcc acaacaggat ctgttttctt gcccatcctt taagggaacac atcaattcat 1500
tttctaattg tcttccctca caagcgggac caggcacagg gcgaggctca tcatgaccc 1560
aagatggcgg ccgggcattt ctcccaggga tctctgtgct tcctttgtg ctctctgtgt 1620
gtgtggatat ttaaaggggc tggaaatgtg caaaaacatg tcaactactta gacattatat 1680
tgtcatcttg ctgtttctag tgatgttaat tatctccatt tcagcagatg tgtggcctca 1740
gatggtaaag tcagcagcct ttcttatttc tcacctggaa atacatacga ccatttgagg 1800
agacaaatgg caaggtgtca gcataccctg aacttgagtt gagagctaca cacaatatta 1860
ttggtttccg agcatcacia acaccctctc tgtttcttca ctgggcacag aattttaata 1920
cttatttcag tgggctgttg gcaggaacaa atgaagcaat ctacataaag tcaatagtgc 1980
agtgcctgac acacaccatt ctcttgaggt cccctctaga gatccacag gtcatatgac 2040
ttcttgggga gcagtggctc acacctgtaa tcccagcact ttgggaggct gaggcaggtg 2100
ggtcacctga ggtcaggagt tcaagaccag cctggccaat atggtgaaac cccatctcta 2160
ctaaaaatc aaaaattagc tgggcgtgct ggtgcatgcc tgtaatccca gcccacac 2220

```

aatggaatt

2229

<210> 470

<211> 2426

<212> DNA

<213> Homo sapiens

<400> 470

gtaaaattcct	tattgccagg	agtgaaccct	aaagtggctc	acaagagtgc	cctattttcct	60
tcaattaact	acaaggacaa	acacatctca	aagttgagat	aagtgaccag	tatgatttgc	120
caaaattcta	aagcgcactc	accatgaaat	ggataaaggt	tacctttggg	gattttgcact	180
gcatgaattc	tgtgaaaagc	ttgttggata	ttgtgataga	gatagagaaa	tgaagtatat	240
tatataagat	actatgaggt	tccctgcctt	tgcttcacat	cccaggctta	caaacgtgcc	300
ccataaacat	tccctctgtg	gctcttgcac	ttcatatatt	tatctaaact	cttataatca	360
aattacactt	ttagtatttg	ctgtctcatg	tgatgatgaa	tctcatatgt	gtcccttctt	420
tgcatgaagt	aagatagtca	acttattcaa	aactttacat	cattctagat	ttaagagaca	480
aggaagagct	tctcaggcag	aaggaataat	gtatgcctga	catgttcaag	gaattacaag	540
ttagattttg	tttaggtgca	tgggaggggt	tgatgggtgat	gacagataag	gctggaggga	600
tggggagagg	ctgtggctgt	atacagcctc	agtacaaggc	taagcatttt	aactttatac	660
tggaaaaaaa	atcaaacaaa	ggggagggat	aaaggactta	gtcatctttg	cactggaaaa	720
caaaatatgt	aattaaattc	ccatagctgc	atgtaacatt	gaattcttcc	agggttaaaaa	780
aaaaagttaa	tcctgtgata	ttaatggaat	gacattttga	ggctctgaga	atgggcacaa	840
aagtgggaaa	tgaatttcag	tatgggcaaa	gacactgagg	atgatgttga	ttagataaatt	900
cactccgtaa	tgatcatgct	gtgtgctagt	aagtataacc	ctggaaagat	cttgagatgc	960
ttcccagcct	gttcacagat	cccctgggcc	agaacactcc	ttaggaaaaa	cagtcagcta	1020
catattaggg	agcaacacga	agggctcttg	aacaaaaatga	gtaatgttat	tctacagtgt	1080
agaaaggtca	cagtacagat	ctgggaacta	aatattaaaa	atgagtgtgg	ctggatatat	1140
ggagaatggt	gggcccagaa	ggaaccgtag	agatcagata	ttacaacagc	ttgtttttga	1200
gggttagaaa	tatgaaatga	tttggttatg	aacgcacagt	ttaggcagca	gggcccagaat	1260
cctgaccctc	tgccccgtgg	ttatctcctc	cccagcttgg	ctgcctcatg	tcacacagct	1320
attccatttt	gtttgttgca	tgtcttgtga	agccatcaag	attttctcgt	ctgttttctt	1380
ctcattggta	atgctcactt	tgtgacttca	tttcaaatct	gtaatccctg	tcaaataaat	1440
atccacaaca	ggatctgttt	tctgccccat	cctttaagga	acacatcaat	tcattttcta	1500
atgtccttcc	ctcacaagcg	ggaccaggca	cagggcgagg	ctcatcgatg	acccaagatg	1560
gcggccgggc	atttctccca	gggatctctg	tgcttccctt	tgtgcttcct	gtgtgtgtgg	1620
atattttaaag	gggctggaaa	tgtgcaaaaa	catgtcacta	cttagacatt	atattgtcat	1680
cttgctgttt	ctagtgatgt	taattatctc	catttcagca	gatgtgtggc	ctcagatggg	1740
aaagtcagca	gcctttctta	tttctcacct	ggaaatacat	acgaccattt	gaggagacaa	1800
atggcaaggt	gtcagcatac	cctgaacttg	agttgagagc	tacacacaat	attattgggt	1860
tccgagcatc	acaaacaccc	tctctgtttc	ttcactgggc	acagaatttt	aatacttatt	1920
tcagtgggct	gttggcagga	acaaatgaag	caatctacat	aaagtcacta	gtgcagtgcc	1980
tgacacacac	cattctcttg	aggteccctc	tagagatccc	acaggtcata	tgacttcttg	2040
gggagcagtg	gctcacacct	gtaatcccag	cactttggga	ggctgaggca	ggtgggtcac	2100
ctgaggtcag	gagttcaaga	ccagcctggc	caatatgggtg	aaaccccatc	tctactaaaa	2160
atacaaaaat	tagctgggag	tgctgggtgca	tgctgttaat	cccagctact	tgggaggctg	2220
aggcaggaga	attgctggaa	catgggaggc	ggagggttga	gtgagctgta	attgtgccat	2280
tgactcga	cctgggagac	agagtggaa	tctgtttcca	aaaaacaaac	aaacaaaaaa	2340
ggcatagtca	gatacaacgt	gggtgggag	tgtaaataga	agcaggatat	aaagggcag	2400
gggtgacggt	tttgcacca	acaatg				2426

<210> 471

<211> 812

<212> DNA

<213> Homo sapiens

<400> 471

gaacaaaatg	agtaatgtta	ttctacagtg	tagaaaggctc	acagtacaga	tctgggaact	60
aaatattaaa	aatgagtgtg	gctggatata	tggagaatgt	tgggcccaga	aggaaccgta	120

```

gagatcagat attacaacag ctttgttttg aggggtagaa atatgaaatg atttggttat 180
gaacgcacag tttaggcagc agggccagaa tcctgaccct ctgccccgtg gttatctcct 240
ccccagcttg gctgcctcat gtcacacag tattccattt tgtttggtgc atgtcttggt 300
aagccatcaa gattttctcg tctgttttcc tctcattggt aatgctcact ttgtgacttc 360
atttcaaate tgtaatcccc ttcaaataaa tatccacaac aggatctgtt ttctgcccc 420
tcctttaagg aacacatcaa ttcatTTTTt aatgtccttc cctcacaagc gggaccagge 480
acagggcgag gctcatcgat gacccaagat ggcggccggg catttctccc agggatctct 540
gtgcttctct ttgtgcttcc tgtgtgtgtg gatatttaaa ggggctggaa atgtgcaaaa 600
acatgtcact acttagacat tatattgtca tcttgtgtgt tctagtgtat ttaattatct 660
ccatttcagc agatgtgtgg cctcagatgg taaagtcagc agcctttctt atttctcacc 720
tctgtatcat caggctcttc ccaccatgca gatcttctcg gtctccctcg gctgcagcca 780
caciaaatctc cctctgttt ttctgatgcc ag
812

```

<210> 472

<211> 515

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)... (515)

<223> n = A,T,C or G

<400> 472

```

acggagactt attttctgat attgtctgca tatgtatgtt tttaagagtc tggaaatagt 60
cttatgactt tcctatcatg cttattaata aataatacag cccagagaag atgaaaatgg 120
gttcagaat tattggctct tgcagcccg tgaatctcag caagaggaac caccaactga 180
caatcaggat attgaacctg gacaagagag agaaggaaca cctccgatcg aagaacgtaa 240
agtagaaggt gattgccagg aaatggatct ggaaaagact cggagtgagc gtggagatgg 300
ctctgatgta aaagagaaga ctccaccta tcctaagcat gctaagacta aagaagcagg 360
agatgggcag ccataagtta aaaagaagac aagctgaagc taacacatg gctgatgtca 420
cattgaaaat gtgactgaaa atttgaaaat tctctcaata aagtttgagt tttctctgaa 480
gaaaaaaaaa naaaaaaaaa aaanaaaan aaaaa
515

```

<210> 473

<211> 5829

<212> DNA

<213> Homo sapiens

<400> 473

```

cgcagccgg ggaagcccaa gctggctcga agagccacca gccacctgtg caaggggtggg 60
cctggaccag ttggaccagc caccaagctc acctactcaa ggaagcaggg atggccagg 120
tgcaacagcc tgagtggctg ccacctgata gctgatggag cagaggcctg aggaaaatca 180
gatggcacat ttagctcttt aatggatctt aagttaattt ttctataaag cacatggcac 240
cagtcctatg ctacagagctc gtatggcact gcggaccaca gcaggccgag ttcccaggat 300
tgccatccag gggggccttc tgtagccctg gccagacctt gcagagggtg ctgggtgctc 360
tttgagcgag ctggcctcc ctggcatgca caggccccag gtactgacac gctgctctga 420
gtgagcttgt cctgccttgg ctgccacctt actgctgatg gagcagcggc cttaggaaaa 480
gcaaatggcg ctgtagccca actttagggt agaagaagat gtacctgtc cggccgctag 540
ttggtgactg gtgcacctgc tcctggcgta cccttgacga ggtgggtggg tgctctttgg 600
ccagcttggc ctgcttggc atgcacaagc ctcagtgcac caactgtcct acaaatggag 660
acacagagag gaaacaagca gcgggctcag gagcagggtg tgtgctgcct ttggggctcc 720
agtccatgcc tcgggtcgta tggtagtgca ggcttcttgg ttgccaagag gcggaccaca 780
ggccttcttg aggaggactt tacgttcaag tgcagaaaag agccaaaatt accatccatg 840
agactaagcc ttctgtggcc ctggcgagac ttaaaatttg tgccaaggca ggacaagctc 900
actcggagca gcgtgtcagt agctggggcc tatgcatgcc gggcagggcc gggctggctg 960
aaggagcaac cagccacctc tgcaagggtg cgcctagtgc aggcggagca tccaccacct 1020
caccgcctcg aggaagtggg gatggccagg ttcccacagc ctgagtgtct gccaccttat 1080

```

tgctgatgga	gcagaggcct	taagaaaagc	agatggcact	gtggccctac	ctttagggtg	1140
gaagaagtga	tgtacatgtc	cggacgctaa	ttggtgactg	gtacaccggc	tcctgctaca	1200
cctttgcaga	ggtggctggt	tgctctttga	gccagcttgt	ccttgcccgg	catgcacaag	1260
tttcagtga	acaactttgc	cacaaatgga	gccatataga	ggaaacaaga	agcagggtca	1320
ggagaagggg	gtaccctgcc	tttggggctc	cagtccatgc	ctcagggtgc	acatggcact	1380
gcgggcttct	tggttgccag	gaggcggacc	acaggccatc	ttggggagga	ctttgtgttc	1440
aagtgcagaa	agcagccagg	attgccatcc	agggggacct	tctatagccc	tggccaaacc	1500
ttgcaggggt	gtctgggtgc	tctttgagcc	ggcttggcct	ccctggcatg	cacggggccc	1560
agggtctggc	acgctgctcc	gagtgtgctt	gtcctgcctt	ggctgccacc	tctgcggggg	1620
tgcgctctgga	gggggtggac	cggccaccaa	ccttaccag	tcaagggaagt	ggatggccat	1680
gttcccacag	cctgagtggc	tgccacctga	tggtgatgg	agcaaaggcc	ttaggaaaag	1740
cagatggccc	ttggccctac	ctttttgtta	gaagaactga	tgttccatgt	cctgcagcga	1800
gtgaggttgg	tggctgtgcc	cccagctcct	ggcgcgccct	cgcagagggt	actgggtgct	1860
ctttggggccc	tcttggcctt	gcccagcatg	cacaagcctc	agtgtacta	ctgtgctaca	1920
aatggagcca	tataggggaa	acgagcagcc	atctcaggag	caagggtgat	gctgcctttg	1980
ggggctccag	tccttgcttc	aagggtctta	tgctactgtg	ggcttcttgg	ttgtcaagag	2040
gcagaccata	ggcgtcttg	agagggactt	tatgttcaag	tgcaaaaagc	agccaggatt	2100
gccaccctcg	ggactctgccc	ttctgtggcc	ctggccaaac	ttagaatttg	gccgtagaca	2160
ggacaggctc	acttgagta	gcgtgtccgt	agctgggggtc	tgtgcatgcc	gggcaaggcc	2220
gggctggctc	ggggagcaac	cagccacctc	tgcggggggtg	cgcttgagc	aggtggagca	2280
gccaccagct	caccactcc	aggaagccgg	ggtagccagg	ttcccaaggc	ctgagtgggt	2340
gccacctaat	ggctgaagaa	acagaggcct	tggaaaaacc	agatggcact	gtggccctac	2400
ctttatggta	gaagagctga	tttagcctga	ctggcagcgt	gtgggggttg	tggctgggtc	2460
gcctgtctgt	ggcgcatccg	tgcaaggatg	gctggttgcc	ctttgagcca	gcttgccctt	2520
gcccggcatg	cgcaagcctc	agtgaacaa	ctgtgctgca	aatggggcca	tatagaggaa	2580
aggagcagct	ggctctggag	catggtgtgc	actcccttg	ggccttcagt	ccatgtctca	2640
tgggtcgat	gcactgcgg	gctgtgtgtt	tgccaagagg	cagaccacag	gtcatcttga	2700
ggaggacttt	atgttccagt	ccagaaagca	gccagtggta	ccaccaggg	gacttgtgct	2760
tctgtgcccc	ggccagacgt	agaatttgac	aaagtcagga	cggctctcagt	cagagcgggc	2820
tgctgggtccc	cggggcctgt	gcatgccggg	cagggccggg	ctggcttggg	gagcaagcag	2880
ccacctctgt	taaggggtgtg	cctggagcag	gtggagcagc	caaccaacctc	acgcactgaa	2940
agaagcaggg	atggccagggt	tccaacatcc	tgagtggctg	ccacctgatg	gctgatggag	3000
cagaggcctg	aggaaaagca	gatggcactg	ctttgtagt	ctgttctttg	tctctcttga	3060
tctttttcag	ttaatgtctg	ttttatcaga	gactaggatt	gcaaaccctg	ctcttttttg	3120
ctttccattt	gcttggtaaa	tattctctca	tccttttatt	ttaagcctat	gtgtgtcttt	3180
gcacatgaga	tgggtctcct	gaatacagga	caacaatggg	tctttactct	ttatccaact	3240
tgccagtctg	tgtcttttaa	ctggggcatt	tagccatttt	acattttaagt	ttagtattgt	3300
tacatgtgaa	atztatcctg	tcatgatgtt	gctagctttt	tatttttccc	attagtttgc	3360
agttttcttta	tagtgtcaat	ggtctttaca	attcgatatg	ttttttagt	ggctgggtact	3420
ggtttttcct	ttctacgttt	agtgtctcct	tcaggagctc	ttgtaacaca	agaatgtgga	3480
tttatttctt	gtaaggtaaa	tatgtggatt	tatttcttgg	gactgtattc	tatggccttt	3540
accccaagaa	tcattacttt	ttaaaatgca	attcaaatta	gcataaaaca	tttacagcct	3600
atggaaaggg	ttgtggcatt	agaatcctta	tttataggat	tattttgtgt	ttttttgaga	3660
tatggtcttt	gtcatcgagg	cagaagtgcc	tggttttgat	cataattcac	cacagccctg	3720
aactcttgag	tccaagccat	ccttttgcct	taatctccca	accagttgga	tctgcaggca	3780
taaggcatca	tgcggtggcta	atttttttcac	gttttttttt	tttttttgtc	gagattatgg	3840
tgctactgtg	ttgctctggc	tgatctcaaa	tgtttgacct	caagggatct	ttctgccacg	3900
gcctcctaaa	gtgctaggat	tatatgcatg	atacaccatg	cctattgtag	agtattacat	3960
tattttcaaa	gtcttattgt	aagagccatt	tattgccttt	ggcctaaata	actcaatata	4020
atatctctga	aacttttttt	tgacaaattt	tggggctgga	tgatgagaga	aggggggtttg	4080
aaactttcta	ataagagtta	acttagagcc	atttaagaaa	ggaaaaaaca	caaattatca	4140
gaaaaacaac	agtaagatca	agtgcaaaag	ttctgtggca	aagatgatga	gagtaaaagaa	4200
tatatgtttg	tgactcatgg	tggctttttac	tttgttcttg	aatttctgag	tacgggttaa	4260
catttaaaga	atctacatta	tagataacat	tttattgcaa	gtaaatgtat	ttcaaaattt	4320
gttattgggt	ttgtatgaga	ttattctcag	cctacttcat	tatcaagcta	tattatttta	4380
ttaatgtagt	tcgatgatct	tacagcaaag	ctgaaagctg	tatcttcaaa	atatgtctat	4440
ttgactaaaa	agttattcaa	caggagttaa	tatctataaa	aaaaatacaa	caggaatata	4500
aaaaacttga	ggataaaaaag	atgttggaaa	aagtaattat	aaatcttaaa	aaacatatgg	4560

```

aaactacaca atggtgaaga cacattggtg aagtacaaaa atataaattg gatctagaag 4620
aaagggcaat gcaggcaata gaaaaattag tagaaatccc tttaaagggtt agtttgtaaa 4680
atcaggtaag tttatttata atttgcttct atttatttca ctgcaaatta tattttggat 4740
atgtatatat attgtgcttc ctctgctgtt cttacagcaa ttgacctgc agagttctag 4800
gaaaaagggtg gcatgtgttt ttactttcaa aatattttaa tttccatcat tataacaaaa 4860
tcaatttttc agagtaatga ttctcactgt ggagtcattt gattattaag acccgttggc 4920
ataagattac atcctctgac tataaaaaatc ctggaagaaa acctaggaaa tattcgtctg 4980
gacattgcac ttggcaatga atttatgggt aaccactgat ccacttccag tcaactacca 5040
tgagttttta tttccagata catgaaatca tatgagttga aactttcttt tgattgagca 5100
gtttggaaac cgtctttttg tagaatctgc aagtggatat ttggaaccct ttgaggccta 5160
tgctgaaaaa agaaatatct tcaactacatg atgaccacca gcagcagctg gggaaaccag 5220
caccctgtgg aattccatac ggtgcataga atacatcttc ccttcagtcg gcttgggtca 5280
acttaggtca tgggccacct ggctgatagc agtttccaca gaaatgcttc aagatgaaag 5340
tggatgaccg gggcaccctc caccactgcc ctgtaagacc atgggacaca caggccacca 5400
gttcttttca tgtggtcatc cctgtttaga tgggagaaaa tacacctgcc tcatttttgt 5460
accttctgtg tgaacattcc acggcagact gtcgctaaat gtggatgaag aattgaatga 5520
atgaatgaat atgagagaaa atgaataaat ggttcagatc ctgggctgga aggtctgtga 5580
tgaggatggt gggtagagga gggctctgtt ttcttgctt taagtcacta attgtcactt 5640
tggggcagga gcacaggctt tgaatgcaga ccgactggac tttaattctg gctttactag 5700
ttgtgattgt gtgaccttgt gaaagttact taaacctct gtgctgttt ctttatctgt 5760
aaaatggaga taataagatg tcaaaggact gtggtaaaga ttaaattgctt taaaaaaaaa 5820
aaaaaaaaa

```

<210> 474

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 474

```

atztatggat cattaatgcc tcttttagtag tttagagaaa acgtcaaaaag aaatggcccc 60
agaataagct tcttgatttg taaaattcta tgtcattggc tcaaatttgt atagtatctc 120
aaaatataaa tatatagaca tctcagataa tatatttgaa atagcaaatt cctgttagaa 180
aataatagta cttaactaga tgagaataac aggtcgccat tatttgaatt gtctcctatt 240
cgtttttcat ttgttgtgtt actcatgttt tacttatgag ggatatatat aacttccact 300
gttttcagaa ttattgtatg cagtcagtat gagaatgcaa ttttaagtttc cttgatgctt 360
tttcacactt ctattactag aaataagaat acagtaatat tggcaaagaa aattgaccag 420
ttcaataaaa ttttttagta aatctgattg aaaataaaca ttgcttatgg ctttcttaca 480
tcaatattgt tatgtcctag acaccttatc tgaaattacg gcttcaaaat tctaattatg 540
tgcaaatgtg taaaatatca atactttatg ttcaagctgg ggcctcttca ggcgtcctgg 600
gctgagagag aaagatgcta gctccgcaag ccggagaggg aacaccgcca cattgttaca 660
cggacacacc gccacgtgga cacatgacca gactcacatg tacagacaca cggagacatt 720
accacatgga gacaccgtca cacagtcaca cggacacact ggcatagtca catggacgga 780
cacacagaca tatggagaaa tcacatggac acaccaccac actatcacag ggacacagac 840
acacggagac atcaccacat ggacacactg tcacactacc acagggacac gagacatcac 900
actgtcacat ggacacacca tcacacacat gaacacaccg acacactgcc atatggacac 960
tggcacacac actgccacac tgtcacatgg acacacctcc acaccatcac accaccacac 1020
acactgcctg tggacacaag gacacacaga cactgtcaca gagatacaca aaacactgtc 1080
acacggagac atcaccatgc agatacacca ccactctggg gccgtctgaa ttaccctgct 1140
ggggggacag cagtggcata ctcatgcta agtgactggc tttcacccca gtagtgattg 1200
cctccatca acactgcca ccccagggtg gggctacccc agcccatctt tacaaaacag 1260
ggcaaggtga actaatggag tgggtggagg agttggaaga aatcccagcg tcagtcaccg 1320
ggatagaatt cccaaggaac cctctttttg gaggatgggt tccatttctg gaggcgatct 1380
gccgacaggg tgaatgcctt cttgcttgtc ttctggggaa tcagagagag tccgttttgt 1440
ggtgggaaga gtgtggctgt gtactttgaa ctctgtaaa ttctctgact catgtccaca 1500
aaaccaacag ttttgtgaat gtgtctggag gcaagggaag ggccactcag gatctatgtt 1560
gaagggaaga ggctggggc tggagtattc gctt

```

<210> 475

<211> 2414
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (33)
<223> n=A,T,C or G

<400> 475

```
cccaacacaa tggctttata agaatgcttc acntgtgaaa aacaaatata aaagtcttct 60
tgtagattat ttttaaggac aaatctttat tccatgttta atttatttag ctttccctgt 120
agctaataat tcatgctgaa cacattttta atgctgtaaa tgtagataat gtaatttatg 180
tatcattaat gcctcttttag tagtttagag aaaacgtcaa aagaaatggc ccagaataa 240
gcttcttgat ttgtaaaatt ctatgtcatt ggctcaaatt tgtatagtat ctcaaaatat 300
aaatatatag acatctcaga taatatattt gaaatagcaa attcctgtta gaaaataata 360
gtacttaact agatgagaat aacaggctgc cattatttga attgtctcct attcgttttt 420
catttgttgt gttactcatg ttttacttat ggggggatat atataacttc cgctgttttc 480
agaagtattg tatgcagtca gtatgagaat gcaatttaag tttccttgat gctttttcac 540
acttctatta ctagaaataa gaatacagta atattggcaa agaaaattga ccagttcaat 600
aaaatttttt agtaaatctg attgaaaata aacattgctt atggctttct tacatcaata 660
ttgttatgtc ctagacacct tatctgaaat tacggcttca aaattcta attggtgcaa 720
tgtgtaaaat atcaatactt tatgttcaag ctggggcctc ttcaggcgtc ctgggctgag 780
agagaagatg gctagctccg caagccgggg agggaaacacc gccacattgt tacatggaca 840
caccgccacg tggacacatg accagactca catgtacaga cacacggaga cattaccaca 900
tggagacacc gtcacacagt cacacgagca cactggcata gtcacatgga cggacacaca 960
gacatatgga gaaatcacac tgacacacca ccacactatc acagggacac agacacacgg 1020
agacatcacc acatggacac actgtcacac taccacaggg acacgagaca tcacactgtc 1080
acatggacac accatcacac acatgaacac accgacacac tgccatatgg acaactgccac 1140
acacactgcc acaactgtcac atggacacac ctccatacca tcacaccacc acacacactg 1200
ccatgtggac acaaggacac acagacactg tcacacagat acacaaaaca ctgtcacacg 1260
gagacatcac catgcagata caccaccaca tggacatagc accagacact ctgccacaca 1320
gatacaccac cacacagaaa tgcggacaca ctgccacaca gacaccacca catcgttgcc 1380
acactttcat gtgtcagctg gcggtgtggg cccacgact ctgggctcta atcgagaaat 1440
tacttgagca tatagtgaag gcaaaatttt tttttatttt ctgggtaacc aagcgcgact 1500
ctgtctcaaa aaaagaaaaa aaaagcaata tactgtgtaa tcgttgacag cataattcac 1560
tattatgtag atcggagagc agaggattct gaatgcatga acatatcatt aacatttcaa 1620
tacattactc ataattactg atgaactaaa gagaaaccaa gaaattatgg tgatagttat 1680
attgacctgg agaaatgtag acacaaaaga accgtaagat gagaaatgtg ttaacacagt 1740
ctataagggc atgcaagaat aaaaataggg gagaaaacag gagagttttt caagagcttt 1800
ctggtcattg aagtcaactt gtatcggtta atttttaaaa ggtttattta catgcaataa 1860
actgcacata cttcaattgt acattttggg aattcttggc attttagct ctataaaacc 1920
agcaacatat taaaatagca aacatatcca ttacctttac caccaaagtt ttctgtgtt 1980
ttttctactc actttttcct gcctatcccc ccatctcttc cacaggtaac cactgatcca 2040
cttccagtca ctatccatga gtttttattt ccaaatacat gaaatcatat gaatttctg 2100
tttttctgtg tggagcccaa ggagcaaggg cagaatgagg aacatgatgt ttcttwccga 2160
cagttactca tgacgtctcc atccaggact gaggggggca tccttctcca tctaggactg 2220
ggggcactct tctccatcca gtattggggg tcatccttct ccatccagta ttgggggtca 2280
tcctcctcca tccaggacct gaggggtgtc cttttctgcg cttecttgga tggcagtctt 2340
tcccttcatg tttatagtra cttaccatta aatcactgtg ccgttttttc ctaaaataaa 2400
aaaaaaaaaa aaaa
```

2414

<210> 476
<211> 3434
<212> DNA
<213> Homo sapiens

<400> 476

ctgtgctgca	aatggggcca	tatagaggaa	aggagcagct	ggctctggag	catgggtgtgc	60
actccctttg	ggccttcagt	ccatgtctca	tgggtcgtat	gacactgcgg	gcttgttggg	120
tgccaagagg	cagaccacag	gtcatcttga	ggaggacttt	atgttccagt	ccagaaagca	180
gccagtggta	ccaccacagg	gacttgtgct	tctgtggccc	aggccagacg	tagaatttga	240
caaagtcagg	acgggtctcag	tcagagcagc	atgtcgggtcc	ccggggcctg	tgcatgccgg	300
gcaggggccag	gctggcttaa	ggagcaagca	gccacctctg	ttaggggtgt	gcctggagca	360
ggtggagcag	ccaccaacct	cacgcactga	aagaagcagg	gatggccagg	ttccaacatc	420
ctgagtggct	gccacctgat	ggctgatgga	gcagaggcct	gaggaaaagc	agatggcact	480
gctttgtagt	gctgttcttt	gtctctcttg	atctttttca	gttaatgtct	gttttatcag	540
agactaggat	tgcaaaccct	gctctttttt	gctttccatt	tgcttggtaa	atatctctcc	600
atccctttat	tttaagccta	tgtgtgtctt	tgcacatgag	atgggtctcc	tgaatacagg	660
acaacaatgg	gtctttactc	tttatccaac	ttgccagtct	gtgtctttta	actggggcat	720
ttagcccatt	tacatttaag	tttagtattt	gttacatgtg	aaatttatcc	tgctcatgat	780
ttgctagctt	tttatttttc	ccattagttt	gcagtttctt	tatagtgtca	atgggtctta	840
caattcgata	tgttttttgta	gtggctggta	ctggtttttc	ctttctacgt	ttagtgtctc	900
cttcaggagc	tcttgtaaca	caagaatgtg	gatttatttc	ttgtaaggta	aatatgtgga	960
tttattctgg	gactgtattc	tatggccttt	acccaagaa	tcattacttt	taaaaatgca	1020
attcaaatta	gcataaaaca	tttacagcct	atggaaaggc	ttgtggcatt	agaatcctta	1080
tttataggat	tatttttgtgt	ttttttgaga	tatggctctt	gtcatcgagg	cagaagtgcc	1140
gtggtttgat	cataattcac	cacagccctg	aactcttgag	tccaagccat	ccttttgect	1200
taatctccca	accagttgga	tctacaagca	taaggcatca	tgcgtaggta	atttttcac	1260
gttttttttt	tttttgcga	gattatggta	tcactgtgtt	gctctggctg	attctcaatg	1320
tttgacctca	agggatcttt	ctgccacagc	ctcctaaagt	gctaggatta	tatgcatgat	1380
acaccatgcc	tattgtagag	tattacatta	ttttcaaagt	cttattgtaa	gagccattta	1440
ttgccttttg	cctaaataac	tcaatataat	atctctgaaa	cttttttttg	acaaattttg	1500
gggcgtgatg	atgagagaag	ggggtttgaa	actttcta	aagagttaac	ttagagccat	1560
ttaagaaagg	aaaaaacaca	aattatcaga	aaaacaacag	taagatcaag	tgcaaaagtt	1620
ctgtggcaaa	gatgatgaga	gtaaagaata	tatgtttgtg	actcatgggtg	gcttttactt	1680
tgttcttgaa	tttctgagta	cgggttaaca	tttaaagaat	ctacattata	gataacattt	1740
tattgcaagt	aatgtatttt	caaaatttgt	tattggtttt	gtatgagatt	attctcagcc	1800
tacttcatta	tcaagctata	ttattttatt	aatgtagtct	gatgatctta	cagcaaaagct	1860
gaaagctgta	tcttcaaaat	atgtctattt	gactaaaaag	ttattcaaca	ggagtattta	1920
tctataaaaa	aatacaacag	gaatataaaa	aacttgagga	taaaaagatg	ttggaaaaag	1980
taatattaaa	tcttaaaaaa	catatggaaa	ctacacaatg	gtgaagacac	attggtgaag	2040
tacaaaaata	taaattggat	ctagaagaaa	gggcaatgca	ggcaatagaa	aaattagtag	2100
aaatcccttt	aaagggttagt	ttgtaaaatc	aggtaagttt	atttataatt	tgctttcatt	2160
tatttctactg	caaatttatat	tttggatatg	tatatatatt	gtgcttcctc	tgctgtcttt	2220
acaggcaattt	gccttgcaga	gttctagga	aaagggtggca	tggtgtttta	ctttcaaaa	2280
atttaaat	ccatcattat	aacaaaatca	atttttcaga	gtaatgattc	tcactgtgga	2340
gtcattttgat	tattaagacc	cgttggcata	agattacatc	ctctgactat	aaaaatcctg	2400
gaagaaaacc	taggaaatat	tcgtctggac	attgcacttg	gcaatgaatt	tatgggcgct	2460
ttggaatcct	gcagatataa	taatgataat	taaacaaaac	actcagagaa	actgccaacc	2520
ctaggatgaa	gtatattgtt	actgtgcttt	gggattaaaa	taagtaacta	cagtttatag	2580
aacttttata	ctgatacaca	gacactaaaa	agggaaaggg	tttagatgag	aagctctgct	2640
atgcaatcaa	gaatctcagc	cactcatttc	tgtaggggct	gcaggagctc	cctgtaaaga	2700
gagggttatgg	agtctgtagc	ttcaggtaag	atacttaaaa	cccttcagag	tttctccatt	2760
ttttcccata	gtttcccca	aaagggttatg	acactttata	agaatgcttc	acttgtgaaa	2820
aacaaatate	aaagtcttct	tgtagattat	ttttaaggac	aaatctttat	tccatgttta	2880
atttatttag	ctttccctgt	agctaataat	tcatgctgaa	cacattttta	atgctgtaaa	2940
tgtagataat	gtaatttatg	tatcattaat	gcctctttag	tagtttagag	aaaacgtcaa	3000
aagaaatggc	cccagaataa	gcttcttgat	ttgtaaaatt	ctatgtcatt	ggctcaaatt	3060
tgtatagtat	ctcaaaatat	aaatatatag	acatctcaga	taatatattt	gaaatagcaa	3120
attcctgtta	gaaaataata	gtacttaact	agatgagaat	aacaggctcg	cattatttga	3180
attgtctcct	attcgttttt	catttgttgt	gttactcatg	ttttacttat	gggggggat	3240
atataacttc	cgctgttttc	agaagtattg	tatgcagtca	gtatgagaat	gcaatttaag	3300
tttctttagt	gctttttcac	acttctatta	ctagaaataa	gaatacagta	atattggcaa	3360
agaaaattga	ccagttcaat	aaaatttttt	agtaaactctg	attgaaaata	aaaaaaaaaa	3420
aaaaaaaaaa	aaaa					3434

<210> 477

<211> 140

<212> PRT

<213> Homo sapiens

<400> 477

Met Asp Gly His Thr Asp Ile Trp Arg Asn His Met Asp Thr Pro Pro
5 10 15

His Tyr His Arg Asp Thr Asp Thr Arg Arg His His His Met Asp Thr
20 25 30

Leu Ser His Tyr His Arg Asp Thr Arg His His Thr Val Thr Trp Thr
35 40 45

His His His Thr His Glu His Thr Asp Thr Leu Pro Tyr Gly His Trp
50 55 60

His Thr His Cys His Thr Val Thr Trp Thr His Leu His Thr Ile Thr
65 70 75 80

Pro Pro His Thr Leu Pro Val Asp Thr Arg Thr His Arg His Cys His
85 90 95

Thr Asp Thr Gln Asn Thr Val Thr Arg Arg His His His Ala Asp Thr
100 105 110

Pro Pro Leu Trp Cys Arg Leu Asn Tyr Pro Ala Gly Gly Thr Ala Val
115 120 125

Ala Tyr Ser Cys Leu Ser Asp Trp Leu Ser Pro Gln
130 135 140

<210> 478

<211> 143

<212> PRT

<213> Homo sapiens

<400> 478

Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
5 10 15

Ser His Gly His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
20 25 30

Gly Glu Ile Thr Trp Thr His His His Thr Ile Thr Gly Thr Gln Thr
35 40 45

His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
50 55 60

Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
65 70 75 80

Pro Thr His Cys His Met Asp Thr Gly Thr His Thr Ala Thr Leu Ser
85 90 95

His Gly His Thr Ser Thr Pro Ser His His His Thr His Cys Leu Trp
 100 105 110
 Thr Gln Gly His Thr Asp Thr Val Thr Gln Ile His Lys Thr Leu Ser
 115 120 125
 His Gly Asp Ile Thr Met Gln Ile His His His Ser Gly Ala Val
 130 135 140

<210> 479
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 479
 Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
 5 10 15
 Ser His Glu His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
 20 25 30
 Gly Glu Ile Thr Leu Thr His His His Thr Ile Thr Gly Thr Gln Thr
 35 40 45
 His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
 50 55 60
 Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
 65 70 75 80
 Pro Thr His Cys His Met Asp Thr Ala Thr His Thr Ala Thr Leu Ser
 85 90 95
 His Gly His Thr Ser Ile Pro Ser His His His Thr His Cys His Val
 100 105 110
 Asp Thr Arg Thr His Arg His Cys His Thr Asp Thr Gln Asn Thr Val
 115 120 125
 Thr Arg Arg His His His Ala Asp Thr Pro Pro His Gly His Ser Thr
 130 135 140
 Arg His Ser Ala Thr Gln Ile His His His Thr Glu Met Arg Thr His
 145 150 155 160
 Cys His Thr Asp Thr Thr Thr Ser Leu Pro His Phe His Val Ser Ala
 165 170 175
 Gly Gly Val Gly Pro Thr Thr Leu Gly Ser Asn Arg Glu Ile Thr Trp
 180 185 190
 Thr Tyr Ser Glu Gly Lys Ile Phe Phe Tyr Phe Leu Gly Asn Gln Ala
 195 200 205
 Arg Leu Cys Leu Lys Lys Arg Lys Lys Lys Gln Tyr Thr Val
 210 215 220

<210> 480
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 480
 Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val
 5 10 15
 Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr
 20 25 30
 Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg
 35 40 45
 Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly
 50 55 60
 Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln
 65 70 75 80
 Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys
 85 90 95
 Arg Ala Arg Pro Gly Trp Leu Gly Glu Gln Pro Ala Thr Ser Ala Gly
 100 105 110
 Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu
 115 120 125
 Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly
 130 135 140

<210> 481
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 481
 Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro
 5 10 15
 Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg
 20 25 30
 Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys Ser His Ser
 35 40 45
 Leu Ser Gly Cys His Leu Met Ala Asp Gly Ala Lys Ala Leu Gly Lys
 50 55 60
 Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr Asp Val Pro

```
<210> 482
<211> 143
<212> PRT
<213> Homo sapiens
```

```
<210> 483
<211> 143
<212> PRT
```

<213> Homo sapiens

<400> 483

Met Glu Thr Gln Arg Gly Asn Lys Gln Arg Ala Gln Glu Gln Gly Val
 5 10 15

Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala
 20 25 30

Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp
 35 40 45

Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu
 50 55 60

Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp
 65 70 75 80

Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg
 85 90 95

Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val
 100 105 110

Arg Leu Val Gln Ala Glu His Pro Pro Pro His Pro Leu Glu Glu Val
 115 120 125

Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys
 130 135 140

<210> 484

<211> 30

<212> PRT

<213> Homo Sapien

<400> 484

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
 20 25 30

<210> 485

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 485

gggaagctta tcacctatgt gccgcctctg c

31

<210> 486

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 486

gcgaattctc acgctgagta ttggcc

27

<210> 487

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 487

cccggaattct tagctgccca tccgaacgcc ttcac

36

<210> 488

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 488

gggaagcttc ttccccggct gcaccagctg tgc

33

<210> 489

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 489

Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala

1

5

10

15

Ser Val Ala

<210> 490

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 490

Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys

1

5

10

15

Leu Ser His Ser

20

<210> 491

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 491

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
1 5 10 15
Thr Gly Phe Thr
20

<210> 492

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 492

Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr
1 5 10 15
Leu Ala Ser Leu
20

<210> 493

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 493

Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro
1 5 10 15
Lys Tyr Arg Gly
20

<210> 494

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 494

Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser
1 5 10 15
Leu Met Ile Ser
20

<210> 495

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 495

Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro
1 5 10 15
Phe Pro Asn Gly
20

<210> 496

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 496

Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
1 5 10 15
Pro Pro Pro Pro Ala
20

<210> 497

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 497

Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
1 5 10 15
Ser Val Arg Val
20

<210> 498

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 498

Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val
1 5 10 15
Val Pro Gly Arg
20

<210> 499

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 499

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 1 5 10 15
 Ser Ala Phe Leu
 20

<210> 500

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 500

Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
 1 5 10 15
 Gly Ser Ile Val
 20

<210> 501

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 501

Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met
 1 5 10 15
 Val Ser Ala Ala
 20

<210> 502

<211> 414

<212> DNA

<213> Homo Sapien

<220>

<221> misc_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 502

caccatggag	acaggcctgc	gctggetttt	cctggctcgt	gtgctcaaag	gtgtccaatg	60
tcagtcggtg	gaggagtccg	ggggtcgcct	ggtcacgcct	gggacacctt	tgacantcac	120
ctgtagagtt	tttggaatng	acctcagtag	caatgcaatg	agctgggtcc	gccaggctcc	180
agggaagggg	ctggaatgga	tcggagccat	tgataattgt	ccacantacg	cgacctgggc	240
gaaaggccga	ttnatnattt	ccaaaacctn	gaccacggtg	gatttgaaaa	tgaccagtcc	300
gacaaccgag	gacacggcca	cctatttttg	tggcagaatg	aatactggta	atagtgggtg	360
gaagaatatt	tggggcccag	gcacctggtg	caccgtntcc	tcagggaac	ctaa	414

<210> 503

<211> 379

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<222> (1)...(379)

<223> n = A,T,C or G

<400> 503

atnccgatggt	gcttggtcaa	aggtgtccag	tgtcagtcgg	tggaggagtc	cgggggtcgc	60
ctggtcacgc	ctgggacacc	cctgacactc	acctgcaccg	tntctggatt	ngacatcagt	120
agctatggag	tgagctgggt	ccgccaggct	ccagggaagg	ggctgggnata	catcggtatca	180
ttagtagtag	tggtagattt	tacgcgagct	gggcgaaagg	ccgattcacc	atttccaaaa	240
cctngaccac	ggtggatttg	aaaatcacca	gtttgacaac	cgaggacacg	gccacctatt	300
tntgtgccag	aggggggttt	aattataaag	acatttgggg	cccaggcacc	ctggtcaccg	360
tntccttagg	gcaacctaa					379

<210> 504

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 504

Gly	Phe	Thr	Asn	Tyr	Thr	Asp	Phe	Glu	Asp	Ser	Pro	Tyr	Phe	Lys	Glu
1			5					10					15		
Asn	Ser	Ala													

<210> 505

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 505

Lys	Glu	Asn	Ser	Ala	Phe	Pro	Pro	Phe	Cys	Cys	Asn	Asp	Asn	Val	Thr
1				5				10						15	
Asn	Thr	Ala	Asn												
				20											

<210> 506

<211> 407

<212> DNA

<213> Homo Sapien

<400> 506

atggagacag	gcctgcgctg	gcttctcctg	gtcgtgcgc	tcaaaggtgt	ccagtgtcag	60
tcgctggagg	agtcggggg	tcgcctggtc	acgcctggga	caccctgac	actcacctgc	120
accgtctctg	gattctccct	cagtagcaat	gcaatgatct	gggtccgcca	ggctccaggg	180
aaggggctgg	aatacatcgg	atacattagt	tatgggtgga	gcgcatacta	cgcgagctgg	240
gtgaaaggcc	gattcaccat	ctccaaaacc	tcgaccacgg	tggatctgag	aatgaccagt	300
ctgacaaccg	aggacacggc	cacctatttc	tgtgccagaa	atagtgattt	tagtggtatg	360
ttgtggggcc	caggcacccct	ggtcaccgtc	tcctcagggc	aacctaa		407

<210> 507
 <211> 422
 <212> DNA
 <213> Homo Sapien

<400> 507
 atggagacag gcctgcgctg gcttctcctg tgcgctgtgc tcaaaggtgt ccagtgtcag 60
 tcggtggagg agtccggggg tcgcctgggc acgcctggga caccctgac actcacctgt 120
 acagtctctg gattctccct cagcaactac gacctgaact gggtcgcca ggctccaggg 180
 aaggggctgg aatggatcgg gatcattaat tatgttggtg ggacggacta cgcgaactgg 240
 gcaaaaggcc ggttcacccat ctccaaaacc tcgaccaccg tggatctcaa gatcgccagt 300
 ccgacaaccg aggacacggc cacctatttc tgtgccagag ggtggaagtg cgatgagtct 360
 ggtccgtgct tgcgcattct gggcccaggc accctgggtca ccgtctcctt agggcaacct 420
 aa 422

<210> 508
 <211> 411
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> misc_feature
 <222> (1)...(411)
 <223> n = A,T,C or G

<400> 508
 atggagacag gcctgcgctg cttctcctgg tgcgctgtgc caaaggtgtc cagtgtcagt 60
 cggtggagga gtccgggggt cgcttggtca cgctggggac accctgaca ctcacctgca 120
 cagtctctgg aatcgacctc agtagctact gcatgagctg ggtccgccag gctccaggga 180
 aggggctgga atggatcgga atcattggta ctcttggtga cacatactac gcgaggtggg 240
 cgaaaggccg attcaccatc tccaaaacct cgaccacggg gcatntgaaa atcnccagtc 300
 cgacaaccga ggacacggcc acctatttct gtgccagaga tcttcgggat ggtagtagta 360
 ctggttatta taaaatctgg ggcccaggca cctgggtcac cgtctccttg g 411

<210> 509
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 509
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 1 5 10 15

<210> 510
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in a lab

<400> 510
 Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile
 1 5 10 15

<210> 511
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 511

Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Asp Gln Lys
1 5 10 15

<210> 512
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 512

Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu
1 5 10 15

<210> 513
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 513

Ala Pro Cys Gly Gln Val Gly Val Pro Asx Val Tyr Thr Asn Leu
1 5 10 15

<210> 514
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 514

Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
1 5 10 15

<210> 515
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 515
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg
1 5 10 15

<210> 516
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 516
Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln
1 5 10 15

<210> 517
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 517
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met
1 5 10 15

<210> 518
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 518
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
1 5 10 15

<210> 519
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 519
Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg Asn Tyr Asp Glu Gly Cys
1 5 10 15
Gly

<210> 520
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 520

Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr
1				5				10						15	
Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly							
			20				25								

<210> 521

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 521

Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu	Leu
1				5				10						15	
Pro	Pro	Pro	Pro	Ala											
				20											

<210> 522

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 522

Leu	Leu	Val	Val	Pro	Ala	Ile	Lys	Lys	Asp	Tyr	Gly	Ser	Gln	Glu	Asp
1				5					10					15	
Phe	Thr	Gln	Val												
			20												

<210> 523

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<220>

<221> VARIANT

<222> (1) ... (254)

<223> Xaa = any amino acid

<400> 523

Met	Ala	Thr	Ala	Gly	Asn	Pro	Trp	Gly	Trp	Phe	Leu	Gly	Tyr	Leu	Ile
1				5				10						15	
Leu	Gly	Val	Ala	Gly	Ser	Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile
			20				25					30			
Asn	Gly	Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu
		35					40								45

Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
 50 55 60
 Trp Val Leu Ser Ala Thr His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
 65 70 75 80
 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
 85 90 95
 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
 100 105 110
 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
 115 120 125
 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
 130 135 140
 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
 145 150 155 160
 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
 165 170 175
 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
 180 185 190
 Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser Gly
 195 200 205
 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
 210 215 220
 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
 225 230 235 240
 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 245 250

<210> 524

<211> 765

<212> DNA

<213> Homo sapien

<400> 524

atggccacag	caggaaatcc	ctggggctgg	ttcctgggggt	acctcatcct	tggtgtcgca	460
ggatcgctcg	tctctggtag	ctgcagccaa	atcataaacg	gcgaggactg	cagcccgcac	120
tgcgagccct	ggcaggcggc	actgggtcatg	gaaaacgaat	tggtctgctc	gggcgtcctg	180
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggt	240
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	300
ctctccgtac	ggcaccaga	gtacaacaga	cccttgctcg	ctaacgacct	catgtctatc	360
aagttggacg	aatccgtgtc	cgagtctgac	accatccgga	gcatcagcat	tgcttcgcag	420
tgccctaccg	cggggaactc	ttgcctcggt	tctggctggg	gtctgctggc	gaacggcaga	480
atgcctaccg	tgctgcagtg	cgtgaacgtg	tcgggtgggt	ctgaggaggt	ctgcagtaag	540
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgcgg	gcggagggca	agaccagaag	600
gactcctgca	acgggtgactc	tggggggccc	ctgatctgca	acgggtactt	gcagggcctt	660
gtgtctttcg	gaaaagcccc	gtgtggccaa	gttggtgtgc	caggtgtcta	caccaacctc	720
tgcaaattca	ctgagtggat	agagaaaacc	gtccaggcca	gttaa		765

<210> 525

<211> 254

<212> PRT

<213> Homo sapien

<400> 525

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
 1 5 10 15
 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
 20 25 30
 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu

35	40	45
Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln		
50	55	60
Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly		
65	70	75
Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met		
85	90	95
Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu		
100	105	110
Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu		
115	120	125
Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala		
130	135	140
Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg		
145	150	155
Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu		
165	170	175
Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys		
180	185	190
Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly		
195	200	205
Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly		
210	215	220
Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu		
225	230	235
Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser		
245	250	

<210> 526

<211> 963

<212> DNA

<213> Homo sapiens

<400> 526

```

atgagttcct gcaacttcac acatgccacc tttgtgctta ttggtatccc aggattagag 60
aaagcccat tctgggttgg cttccccctc cttccatgt atgtagtggc aatgtttgga 120
aactgcatcg tgggtcttcat cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180
tttctctgca tgcttgacgc cattgacctg gccttatcca catccaccat gcctaagatc 240
tttgcccttt tctgggttga ttcccgagag attagctttg aggcctgtct taccagatg 300
ttctttatcc atgcctctc agccattgaa tccaccatcc tgctggccat ggcctttgac 360
cgttatgtgg ccatctgcca cccactgcgc catgctgcag tgctcaacaa tacagtaaca 420
gccagattg gcatcgtggc tgtggtccgc ggatccctct ttttttccc actgcctctg 480
ctgatcaagc ggctggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540
caggatgtaa tgaagttggc ctatgcagac actttgccca atgtggtata tgggtcttact 600
gccattctgc tgggtcatggg cgtggacgta atgttcatct ccttgctcta ttttctgata 660
atacgaacgg ttctgcaact gccttccaag tcagagcggg ccaaggcctt tggaacctgt 720
gtgtcacaca ttggtgtggt actcgccttc tatgtgccac ttattggcct ctcagttgta 780
caccgctttg gaaacagcct tcatccatt gtgcgtgttg tcatgggtga catctacctg 840
ctgctgcctc ctgtcatcaa tccatcatc tatggtgccaa aaaccaaaca gatcagaaca 900
cgggtgctgg ctatgttcaa gatcagctgt gacaaggact tgcaggctgt gggagggaag 960
tga
963

```

<210> 527

<211> 320

<212> PRT

<213> Homo sapiens

<400> 527

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
 5 10 15
 Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
 20 25 30
 Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
 35 40 45
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 50 55 60
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
 65 70 75 80
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
 85 90 95
 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
 100 105 110
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
 130 135 140
 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
 145 150 155 160
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 165 170 175
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
 180 185 190
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
 195 200 205
 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
 210 215 220
 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
 225 230 235 240
 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
 245 250 255
 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
 260 265 270
 Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
 275 280 285
 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
 290 295 300
 Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys

305

310

315

320

<210> 528
<211> 20
<212> DNA
<213> Homo Sapien

<400> 528
actatgggtcc agaggctgtg

20

<210> 529
<211> 20
<212> DNA
<213> Homo Sapien

<400> 529
atcacctatg tgccgcctct

20

<210> 530
<211> 1852
<212> DNA
<213> Homo sapiens

<400> 530

ggcacgagaa	ttaaaaccct	cagcaaaaaca	ggcatagaag	ggacatacct	ttaaagtaata	60
aaaaccacct	atgacaagcc	cacagccaac	ataatactaa	atggggaaaa	gttagaagca	120
tttcctctga	gaactgcaac	aataaataca	aggatgctgg	attttgtcaa	atgccttttc	180
tgtgtctgtt	gagatgctta	tgtgactttg	cttttaattc	tgtttatgtg	attatcacat	240
ttattgactt	gcctgtgtta	gaccggaaga	gctgggggtg	ttctcaggag	ccaccgtgtg	300
ctgcggcagc	ttcgggataa	cttgaggctg	catcactggg	gaagaaacac	aytcctgtcc	360
gtggcgctga	tggttgagga	cagagcttca	gtgtggettc	tctgcgactg	gcttcttcgg	420
ggagttcttc	cttcatagtt	catccatagt	gctccagagg	aaaattatat	tattttgtta	480
tggatgaaga	gtattacgtt	gtgcagatat	actgcagtgt	cttcactctc	tgatgtgtga	540
ttgggtaggt	tccaccatgt	tgccgcagat	gacatgattt	cagtacctgt	gtctggtgta	600
aaagtgtttg	tttgtgaatg	gatattgtgg	tttctggatc	tcatectctg	tgggtggaca	660
gctttctcca	ccttgctgga	agtgcctgc	tgtccagaag	tttgatggct	gaggagtata	720
ccatcgtgca	tgcatctttc	atttcctgca	tttcttctc	cctggatgga	cagggggagc	780
ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	gacgcttggg	840
agcaagaggt	gcaagtgggt	ctgccactgc	ttccctgct	gcagggggag	cggcaagagc	900
aacgtggctg	cttggggaga	ctacgatgac	agcgccttca	tggatcccag	gtaccacgtc	960
catggagaag	atctggacaa	gctccacaga	gctgcctggg	ggggtaaaag	ccccagaaag	1020
gatctcatcg	tcatgctcag	ggacacggat	gtgaacaaga	gggacaagca	aaagaggact	1080
gctctacatc	tggcctctgc	caatgggaat	tcagaagtag	taaaactcgt	gctggacaga	1140
cgatgtcaac	ttaatgtcct	tgacaacaaa	aagaggacag	ctctgacaaa	ggccgtacaa	1200
tgccaggaag	atgaatgtgc	gttaatgttg	ctggaacatg	gcactgatcc	aaatattcca	1260
aatgagtatg	gaaataccac	tctacactat	gctgtctaca	atgaagataa	attaatggcc	1320
aaagcactgc	tcttatacgg	tgctgatatc	gaatcaaaaa	acaagcatgg	cctcacacca	1380
ctgctacttg	gtatacatga	gcaaaaaacag	caagtgggtga	aatttttaat	caagaaaaaa	1440
gcgaatttaa	atgcgctgga	tagatatgga	agaactgctc	tcatacttgc	tgtatgttgt	1500
ggatcagcaa	gtatagtcag	ccctctactt	gagcaaaatg	ttgatgtatc	ttctcaagat	1560
ctggaaagac	ggccagagag	tatgctgttt	ctagtcatca	tcatgtaatt	tgccagttac	1620
tttctgacta	caaagaaaaa	cagatgttaa	aaatctcttc	tgaaaacagc	aatccagaac	1680
aagacttaaa	gctgacatca	gaggaagagt	cacaaaaggct	taaaggaagt	gaaaacagcc	1740
agccagagct	agaagattta	tggctattga	agaagaatga	agaacacgga	agtactcatg	1800
tgggattccc	agaaaacctg	actaacggtg	ccgctgctgg	caatggtgat	ga	1852

<210> 531
<211> 879

<400> 531

<210> 532

<211> 292

<212> PRT

<213> Homo sapiens

<400> 532

Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile
165 170 175

Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu
 180 185 190

Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu
 195 200 205

Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Ile His Glu
 210 215 220

Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu
 225 230 235 240

Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys
 245 250 255

Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp
 260 265 270

Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu Phe Leu
 275 280 285

Val Ile Ile Met
 290

<210> 533

<211> 801

<212> DNA

<213> Homo sapiens

<400> 533

atgtacaagc ttcagtgcaa caactgtgct acaaattggag ccacagagag gaaacaagca 60
 gcaggctcag gaggagggtg tgcgtgcct tcggctctcc aatccatgcc tcagggtctcc 120
 tatgccactg cagcattctt ggttgccaag aggccaaacca caggccatct tgagaaggag 180
 tttatgttcc actgcagaaa gcagccagga tcaccatcca ggggacttgg tcttctgttg 240
 ccctggccag acatagaatt tgtgccaagg caggacaagc tcaactcagag cagcgtgtta 300
 gtacctcaaa tctgtgcgtg ccagacaagg ccaaactggc tcaatgagca accagccacc 360
 tctgcagggg tgcgtctgga ggaggtggac cagccaccaa ccttaccag tcaagggaagt 420
 ggatggccat gttccacacag cctgagtggc tgccacctga tggctgatat agcaaaaggcc 480
 ttaggaaaag cagatggccc ttggccctac ctttttggtta gaagaactga tgttccatgt 540
 cctgcagcga gtgaggttgg tggctgtgcc cccagctcct ggcacaccct cgcagagggtg 600
 actgggttgc ctttgagccc tcttagcctt gccagcatg cacaagcctc agtgctacta 660
 ctgtgctaca aatggagcca tataggggaa acgagcagcc atctcaggag caagggtgtat 720
 gctgcctttg ggggctccag tccttgcttc aagggtctta tgtcactgtg ggcttcttgg 780
 ttgccaagag gcagaccata g 801

<210> 534

<211> 266

<212> PRT

<213> Homo sapiens

<400> 534

Met Tyr Lys Leu Gln Cys Asn Asn Cys Ala Thr Asn Gly Ala Thr Glu
 5 10 15

Arg Lys Gln Ala Ala Gly Ser Gly Ala Gly Tyr Ala Leu Pro Ser Ala
 20 25 30

Leu Gln Ser Met Pro Gln Gly Ser Tyr Ala Thr Ala Arg Phe Leu Val
 35 40 45
 Ala Lys Arg Pro Thr Thr Gly His Leu Glu Lys Glu Phe Met Phe His
 50 55 60
 Cys Arg Lys Gln Pro Gly Ser Pro Ser Arg Gly Leu Gly Leu Leu Trp
 65 70 75 80
 Pro Trp Pro Asp Ile Glu Phe Val Pro Arg Gln Asp Lys Leu Thr Gln
 85 90 95
 Ser Ser Val Leu Val Pro Gln Ile Cys Ala Cys Gln Thr Arg Pro Asn
 100 105 110
 Trp Leu Asn Glu Gln Pro Ala Thr Ser Ala Gly Val Arg Leu Glu Glu
 115 120 125
 Val Asp Gln Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys
 130 135 140
 Ser His Ser Leu Ser Gly Cys His Leu Met Ala Asp Ile Ala Lys Ala
 145 150 155 160
 Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr
 165 170 175
 Asp Val Pro Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser
 180 185 190
 Ser Trp His Thr Leu Ala Glu Val Thr Gly Cys Ser Leu Ser Pro Leu
 195 200 205
 Ser Leu Ala Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys
 210 215 220
 Trp Ser His Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr
 225 230 235 240
 Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu
 245 250 255
 Trp Ala Ser Trp Leu Pro Arg Gly Arg Pro
 260 265

<210> 535

<211> 6082

<212> DNA

<213> Homo sapiens

<400> 535

cctccactat tacagcttat aggaaattac aatccacttt acaggcctca aagggttcatt 60
 ctggccgagc ggacaggcgt ggcggccgga gccccagcat ccttgcttga ggtccaggag 120
 cggagcccg cggcactgcc gctgatcag cgcgaccccg gcccgcgccc gccccgccc 180
 gcaagatgct gcccgtgtac caggaggtga agcccaaccc gctgcaggac gcgaacctct 240
 gctcacgcgt gttcttctgg tggctcaatc ccttggttaa aattggccat aaacggagat 300

tagaggaaga	tgatatgtat	tcagtgtctgc	cagaagaccg	ctcacagcac	cttgggagagg	360
agttgcaagg	gttctgggat	aaagaagttt	taagagctga	gaatgacgca	cagaagcctt	420
ctttaacaag	agcaatcata	aagtgttact	ggaaatctta	tttagttttg	ggaattttta	480
cgttaattga	ggaaagtgcc	aaagtaatcc	agcccatatt	tttgggaaaa	attattaatt	540
attttgaaaa	ttatgatccc	atggattctg	tggctttgaa	cacagcgtac	gcctatgcc	600
cgggtgctgac	tttttgcacg	ctcatttttg	ctatactgca	tcacttatat	ttttatcacg	660
ttcagtgtgc	tgggatgagg	ttacgagtag	ccatgtgcc	tatgatttat	cgggaaggcac	720
ttcgtcttag	taacatggcc	atggggaaga	caaccacagg	ccagatagtc	aatctgctgt	780
ccaatgatgt	gaacaagttt	gatcaggtga	cagtgttctt	acacttcctg	tgggcaggac	840
cactgcaggc	gatcgacgtg	actgccctac	tctggatgga	gataggaata	tcgtgccttg	900
ctgggatggc	agttctaate	attctcctgc	ccttgcaaag	ctgttttggg	aagttgttct	960
catcactgag	gagtaaaact	gcaactttca	cggatgccag	gatcaggacc	atgaatgaag	1020
ttataactgg	tataaggata	ataaaaatgt	acgcctggga	aaagtcattt	tcaaactctta	1080
ttaccaattt	gagaaagaag	gagatttcca	agattctgag	aagttcctgc	ctcaggggga	1140
tgaattttggc	ttcgtttttc	agtgaagca	aaatcatcgt	gtttgtgacc	ttcaccacct	1200
acgtgtcctc	cggcagtggt	atcacagcca	gccgcgtgtt	cgtggcagtg	acgctgtatg	1260
gggctgtgcg	gctgacgggt	accctcttct	tcccctcagc	cattgagagg	gtgtcagagg	1320
caatcgtag	catccgaaga	atccagacct	ttttgctact	tgatgagata	tcacagcgca	1380
accgtcagct	gccgtcagat	ggtaaaaaga	tgggtgcatgt	gcaggatttt	actgcttttt	1440
gggataaggc	atcagagacc	ccaactctac	aaggcctttc	ctttactgtc	agacctggcg	1500
aattgttagc	tgtggtcggc	cccggtggag	caggggaagtc	atcactgtta	agtgcctgtc	1560
tcggggaatt	ggccccaagt	cacgggctgg	tcagcgtgca	tggagaatt	gcctatgtgt	1620
ctcagcagcc	ctgggtgttc	tcgggaactc	tgaggagtaa	tattttattt	gggaagaatt	1680
acgaaaagga	acgatatgaa	aaagtcataa	aggcttgtgc	tctgaaaaag	gatttacagc	1740
tgttggagga	tggtgatctg	actgtgatag	gagatcgggg	aaccacgctg	agtgaggggc	1800
agaaagcag	ggtaaaccct	gcaagagcag	tgtatcaaga	tgtgacatc	tatctcctgg	1860
acgatcctct	cagtgcagta	gatgcggaag	ttagcagaca	cttggttcgaa	ctgtgtattt	1920
gtcaaatatt	gcatgagaag	atcacaattt	tagtgactca	tcagttgcag	tacctcaaag	1980
ctgcaagtca	gattctgata	ttgaaagatg	gtaaaatggg	gcagaagggg	acttacactg	2040
agttccttaa	atctgggtata	gattttggct	cccttttaaa	gaaggataat	gaggaaagtg	2100
aacaacctcc	agttccagga	actccacac	taaggaaatcg	taccttctca	gagtcctcgg	2160
tttgggtctca	acaatcttct	agacctcct	tgaaagatgg	tgctctggag	agccaagata	2220
cagagaatgt	cccagttaca	ctatcagagg	agaaccgttc	tgaaggaaaa	gttgggttttc	2280
aggcctataa	gaattacttc	agagctgggt	ctcactggat	tgtcttcatt	ttccttatte	2340
tcctaaacac	tgcagctcag	gttgccctatg	tgttcaaga	ttgggtggctt	tcatactggg	2400
caaacaacaa	aagtatgcta	aatgtcactg	taaatggagg	aggaaatgta	accgagaagc	2460
tagatcttaa	ctgggtactta	ggaatttatt	cagggttaac	tgtagctacc	gttctttttg	2520
gcatagcaag	atctctattg	gtattctacg	tccttggttaa	ctcttcacaa	actttgcaca	2580
acaaaatggt	tgagtcaatt	ctgaaagctc	cggattattt	ctttgataga	aatccaatga	2640
gaagaatttt	aaatcgtttc	tccaaagaca	ttggacactt	ggatgatttg	ctgccgctga	2700
cgtttttaga	tttcatccag	acattgctac	aagtgggttg	tgtggtctct	gtggctgtgg	2760
ccgtgattcc	ttggatcgca	atacccttgg	ttcccttggg	aatcattttc	atttttcttc	2820
ggcgatattt	tttggaaacg	tcaagagatg	tgaagcgctt	ggaatctaca	actcggagtc	2880
cagtgttttc	ccacttgtca	tcttctctcc	aggggctctg	gaccatccgg	gcatacaaag	2940
cagaagagag	gtgtcaggaa	ctgtttgatg	cacaccagga	tttacattca	gaggcttggg	3000
tcttggtttt	gacaacgtcc	cgctgggttc	cggtccgtct	ggatgccatc	tgtgccatgt	3060
ttgtcatcat	cgttgccctt	gggtccctga	ttctggcaaa	aactctggat	gccgggcagg	3120
ttggtttggc	actgtcctat	gccctcacgc	tcattgggat	gtttcagtgg	tgtgttcgac	3180
aaagtgtgta	agttgagaat	atgatgatct	cagtagaaag	ggtcattgaa	tacacagacc	3240
ttgaaaaaga	agcaccttgg	gaatatcaga	aacgcccacc	accagcctgg	ccccatgaag	3300
gagtgataat	ctttgacaat	gtgaacttca	tgtacagctc	aggtgggcct	ctgggtactga	3360
agcatctgac	agcactcatt	aaatcacaa	aaaagggttg	cattgtggga	agaaccggag	3420
ctggaaaaag	ttccctcate	tcagcccttt	ttagattgtc	agaaccggaa	ggtaaaattt	3480
ggattgataa	gatcttgaca	actgaaattg	gacttcacga	tttaagggaag	aaaatgtcaa	3540
tcatacctca	ggaacctgtt	ttgttcaactg	gaacaatgag	gaaaaacctg	gatcccttta	3600
atgagcacac	ggatgaggaa	ctgtggaatg	ccttacaaga	ggtacaactt	aaagaaacca	3660
ttgaagatct	tcctggtaaa	atggatactg	aattagcaga	atcaggatcc	aattttagtg	3720
ttggacaaa	acaactgggtg	tgccttgcca	gggcaattct	caggaaaaat	cagatattga	3780

```

ttattgatga agcgacggca aatgtggatc caagaactga tgagttaata caaaaaaaat 3840
ccgggagaaa tttgcccact gcaccgtgct aaccattgca cacagattga acaccattat 3900
tgacagcgac aagataatgg ttttagattc aggaagactg aaagaatatg atgagccgta 3960
tggtttgctg caaaataaag agagcctatt ttacaagatg gtgcaacaac tgggcaaggc 4020
agaagccgct gccctcactg aaacagcaaa acagggtatac ttcaaaagaa attatccaca 4080
tatttggtcac actgaccaca tggttacaaa cacttccaat ggacagccct cgaccttaac 4140
tattttcgag acagcactgt gaatccaacc aaaatgtcaa gtccgttccg aaggcatttg 4200
ccactagttt ttggactatg taaaccacat tgtacttttt tttacttttg caacaaatat 4260
ttatacatat aagatgctag ttcatttgaa tatttctccc aacttatcca aggatctcca 4320
gctctaacaa aatggtttat ttttatttaa atgtcaatag ttgtttttta aaatccaaat 4380
cagaggtgca ggccaccagt taaatgccgt ctatcagggt ttgtgcctta agagactaca 4440
gagtcaaagc tcatttttaa aggagtagga cagagttgtc acaggttttt gttgttggtt 4500
ttattgcccc caaaattaca tgtaatttc catttatatc agggattcta tttacttgaa 4560
gactgtgaag ttgccatttt gtctcattgt tttctttgac ataactagga tccattattt 4620
cccctgaagg cttcttgtaa gaaaatagta cagttacaac caataggaac aacaaaaaga 4680
aaaagtttgt gacattgtag tagggagtgt gtaccctta ctcccatca aaaaaaaaaa 4740
tggtacatag gttaaaggat agaagggcaa tattttatca tatgttctaa aagagaagga 4800
agagaaaata ctactttctc aaaatggaag cccttaaagg tgctttgata ctgaaggaca 4860
caaatgtgac cgtccatcct ccttttagagt tgcattgact ggacacggta actgttgtag 4920
tttttagactc agcattgtga cacttcccaa gaaggccaaa cctctaaccg acattcctga 4980
aatacgtggc attattcttt tttggatttc tcatttatgg aaggctaacc ctctgttgac 5040
tgtaagcctt ttggtttggg ctgtattgaa atcctttcta aattgcatga ataggctctg 5100
ctaacgtgat gagacaaact gaaaattatt gcaagcattg actataatta tgcagtacgt 5160
tctcaggatg catccagggg ttcattttca tgagcctgtc caggttagtt tactcctgac 5220
cactaatagc attgtcattt gggctttctg ttgaatgaat caacaaacca caatacttcc 5280
tggaaccttt tgtactttat ttgaactatg agtctttaat ttttctgat gatggtgggt 5340
gtaatatggt gatttcagtt tactaaaggt tttactatta tggtttgaag tggagtctca 5400
tgacctctca gaataagggt tcacctcctt gaaattgcat atatgtatat agacatgcac 5460
acgtgtgcat ttgtttgtat acatatattt gtccttcgta tagcaagttt tttgctcacc 5520
agcagagagc aacagatggt ttattgagtg aagccttaaa aagcacacac cacacacagc 5580
taactgccaa aatacattga ccgtagtagc tgttcaactc ctagtactta gaaatacacg 5640
tatggttaat gttcagttca acaaaccaca cacagtaaat gtttattaat agtcatgggt 5700
cgtatttttag gtgactgaaa ttgcaacagt gatcataatg aggtttgtta aaatgatagc 5760
tatattcaaa atgtctatat gtttatttgg acttttgagg ttaaagacag tcatataaac 5820
gtcctgtttc tgttttaatg ttatcataga attttttaat gaaactaaat tcaattgaaa 5880
taaagatag ttttcatctc caaaaaaaaaa aaaaaaaagg gcggccgctc gagtctagag 5940
ggcccggtta aaccgctga tcagcctcga ctgtgccttc tagttgccag ccactctgtt 6000
tttgcccttc ccccgctgct tccttgacct tggaagggtg cactccctact gtcctttcct 6060
aataaaatga ggaaattgca tc
6082

```

<210> 536

<211> 6140

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (4535)

<223> n=A,T,C or G

<400> 536

```

cagtggcgca gtctcagctc actgcagcct ccacctcctg tgttcaagca gtcctcctgc 60
ctcagccacc agactagcag gtctcccccg cctctttctt ggaaggacac ttgccattgg 120
atthagacc cacttggaata atccaggatg atgtcttcac tccaacatcc tcagtttaat 180
tccatgtgca aatacccttt tcccaataaa cattcaattc tttaccagga aagggtggctc 240
aatcccttgt ttaaaattgg ccataaacgg agattagagg aagatgatat gtattcagtg 300
ctgccagaag accgctcaca gcaccttgga gaggagttgc aagggttctg ggataaagaa 360
gttttaagag ctgagaatga cgcacagaag cttcttttaa caagagcaat cataaagtgt 420

```

tactggaaat	cttatttagt	tttgggaatt	tttacgttaa	ttgaggaaag	tgccaaagta	480
atccagccca	tatttttggg	aaaaattatt	aattattttg	aaaattatga	tcccatggat	540
tctgtggctt	tgaacacagc	gtacgcctat	gccacgggtg	tgactttttg	cacgctcatt	600
ttggctatac	tgcatacact	atatttttat	cacgttcagt	gtgctgggat	gaggttacga	660
gtagccatgt	gccatatgat	ttatcggaag	gcacttcgtc	ttagtaacat	ggccatgggg	720
aagacaacca	caggccagat	agtcaatctg	ctgtccaatg	atgtgaacaa	gtttgatcag	780
gtgacagtgt	tcttacactt	cctgtgggca	ggaccactgc	aggcgatcgc	agtgactgcc	840
ctactctgga	tggagatagg	aatatcgtgc	cttgctggga	tggcagttct	aatcattctc	900
ctgcccttgc	aaagctgttt	tgggaagtgt	ttctcatcac	tgaggagtaa	aactgcaact	960
ttcacggatg	ccaggatcag	gaccatgaat	gaagttataa	ctggtataag	gataataaaa	1020
atgtacgcct	gggaaaagtc	attttcaa	cttattacca	at ttgagaaa	gaaggagatt	1080
tccaagattc	tgagaagtgc	ctgcctcagg	gggatgaatt	tggttcgtt	tttcagtgc	1140
agcaaaatca	tctgtttgt	gaccttcacc	acctacgtgc	tcctcggcag	tgtgatcaca	1200
gccagccg	tggtcgtggc	agtgacgctg	tatggggctg	tgcggtcgc	ggttaccctc	1260
ttcttccct	cagccattga	gaggggtgtc	gaggcaatcg	tcagcatccg	aagaatccag	1320
acctttttgc	tacttgatga	gatatacacag	cgcaaccgtc	agctgccgtc	agatggtaaa	1380
aagatgggtg	atgtgcagga	ttttactgct	ttttgggata	aggcatcaga	gaccccaact	1440
ctacaaggcc	tttcttttac	tgtcagacct	ggcgaattgt	tagctgtggt	cggccccgtg	1500
ggagcagggg	agtcatacact	gttaagtgcc	gtgctcgggg	aattggcccc	aagtcacggg	1560
ctggtcagcg	tgcatggaag	aattgcctat	gtgtctcagc	agccctgggt	gttctcggga	1620
actctgagga	gtaatatatt	at ttgggaag	aaatacgaaa	aggaacgata	tgaaaaagtc	1680
ataaaggctt	gtgctctgaa	aaaggattta	cagctgttgg	aggatggtga	tctgactgtg	1740
ataggagatc	ggggaaccac	gctgagtgga	gggcgaagaag	cacgggtaaa	ccttgcaaga	1800
gcagtgtatc	aagatgctga	catctatctc	ctggacgatc	ctctcagtgc	agtagatgcg	1860
gaagttagca	gacacttggt	cgaactgtgt	at ttgtcaaa	ttttgcatga	gaagatcaca	1920
at tttagtga	ctcatcagtt	gcagtacctc	aaagctgcaa	gtcagattct	gatattgaaa	1980
gatggtaaaa	tggtgcagaa	ggggacttac	actgagttcc	taaaatctgg	tatagatttt	2040
ggctcccttt	taaagaagga	taatgaggaa	agtgaacaac	ctccagttcc	aggaactccc	2100
acactaagga	atcgtacctt	ctcagagtct	tcggtttggt	ctcaacaatc	ttctagaccc	2160
tccttgaaa	atggtgctct	ggagagccaa	gatacagaga	atgtcccagt	tacactatca	2220
gaggagaacc	gttctgaagg	aaaagtgggt	tttcaggcct	ataagaatta	cttcaagatc	2280
ggtgctcact	ggattgtctt	cattttccct	attctcctaa	acactgcagc	tcagggtgcc	2340
tatgtgcttc	aagattgggtg	gctttcatac	tgggcaaaca	aacaaagtat	gctaaatgtc	2400
actgtaaatg	gaggaggaaa	tgtaacccag	aaagctagatc	ttaactggta	cttaggaatt	2460
tattcagggtt	taactgtagc	taccgttctt	tttggcatag	caagatctct	attgggtattc	2520
tacgtccttg	ttaactcttc	acaaaactttg	cacaacaaaa	tgtttgagtc	aattctgaaa	2580
gctccggtat	tattctttga	tagaaatcca	ataggaagaa	ttttaaatcg	tttctccaaa	2640
gacattggag	acttggtatga	tttgctgccc	ctgacgtttt	tagatttcat	ccagacattg	2700
ctacaagtgc	ttggtgtggt	ctctgtggct	gtggccgtga	ttccttggtat	cgacaatacc	2760
ttggttcccc	ttggaatcat	tttcattttt	cttcggcgat	at tttttggg	aacgtcaaga	2820
gatgtgaagc	gcctggaatc	tacaactcgg	agtccagtgt	tttcccactt	gtcatcttct	2880
ctccaggggc	tctggaccat	ccgggcatac	aaagcagaag	agaggtgtca	ggaactgttt	2940
gatgcacacc	aggatttaca	ttcagaggct	tgggtcttgt	ttttgacaac	gtcccgtggtg	3000
ttcgccgtcc	gtctggatgc	catctgtgcc	atggtttgtca	tcatacgtgc	ctttgggtcc	3060
ctgattcttg	caaaaactct	ggatgccggg	caggtttggtt	tggcactgtc	ctatgccctc	3120
acgtcatggt	ggatgtttca	gtggtgtggt	cgacaaagtg	ctgaagttga	gaatatgatg	3180
atctcagtag	aaagggtcat	tgaatacaca	gaccttgaaa	aagaagcacc	ttgggaatat	3240
cagaaacgcc	caccaccagc	ctggccccat	gaaggagtga	taatctttga	caatgtgaac	3300
ttcatgtaca	gtccagggtg	gcctctggta	ctgaagcatc	tgacagcact	cattaaatca	3360
caagaaaagg	ttggcattgt	gggaagaacc	ggagctggaa	aaagttccct	catctcagcc	3420
cttttttagat	tgtcagaacc	cgaaggtaaa	at ttggattg	ataagatctt	gacaactgaa	3480
attggacttc	acgatttaag	gaagaaaatg	tcaatcatac	ctcaggaacc	tgttttgttc	3540
actggaacaa	tgaggaaaaa	cctggatccc	tttaatgagc	acacggatga	ggaactgtgg	3600
aatgccttac	aagagggtaca	acttaaagaa	accattgaag	atcttcctgg	taaaatggat	3660
actgaattag	cagaatcagg	atccaatttt	agtgttggac	aaagacaact	ggtgtgcctt	3720
gccagggcaa	ttctcaggaa	aaatcagata	ttgattattg	atgaagcgac	ggcaaatgtg	3780
gatccaagaa	ctgatgagtt	aatacaaaaa	aaaatccggg	agaaatttgc	ccactgcacc	3840
gtgctaacca	ttgcacacag	attgaacacc	attattgaca	gcgacaagat	aatggtttta	3900

```

gattcaggaa gactgaaaga atatgatgag ccgtatgttt tgctgcaaaa taaagagagc 3960
ctatttttaca agatggtgca acaactgggc aaggcagaag ccgctgccct cactgaaaca 4020
gcaaaacaga gatggggttt caccatgttg gccaggctgg tctcaaactc ctgacctcaa 4080
gtgatccacc tgccttggcc tcccaaactg ctgagattac aggtgtgagc caccacgccc 4140
agcctgagta tacttcaaaa gaaattatcc acatattggt cacactgacc acatggttac 4200
aaacacttcc aatggacagc cctcgacctt aactattttc gagacagcac tgtgaatcca 4260
accaaaatgt caagtccgtt ccgaaggcat ttgccactag tttttggact atgtaaacca 4320
cattgtactt ttttttactt tggcaacaaa tatttatata tacaagatgc tagttcattt 4380
gaatatttct cccaacttat ccaaggatct ccagctctaa caaaatgggtt tttttttatt 4440
taaagtcaa tagtkgkttt ttaaaatcca aatcagaggt gcaggccacc agttaaatgc 4500
cgtctatcag gttttgtgcc ttaagagact acagnagtca gaagctcatt tttaaaggag 4560
taggacagag ttgtcacagg tttttgttgg tgtttktatt gcccccaaaa ttacatgtta 4620
atttccattt atatcagggg attctattta cttgaagact gtgaagttgc cattttgtct 4680
cattgttttc tttgacatam ctaggatcca ttatttcccc tgaaggcttc ttgkagaaaa 4740
tagtacagtt acaaccaata ggaactamca aaaagaaaaa gtttgtgaca ttgtagtagg 4800
gagtgtgtac cccttactcc ccatcaaaaa aaaaaatgga tacatgggta aaggatagaa 4860
gggcaatatt ttatcatatg ttctaaaaga gaaggaagag aaaatactac tttctcaaaa 4920
tggaagccct taaagggtgct ttgatactga aggacacaaa tgtgaccgtc catcctcctt 4980
tagagttgca tgaacttgac acggtaactg ttgcagtttt agactcagca ttgtgacact 5040
tccaagaag gccaaacctc taaccgacat tctgaaata cgtggcatta ttcttttttg 5100
gattttctcat ttaggaaggc taaccctctg ttgamgtgam kccttttggg ttgggctgta 5160
ttgaaatcct ttctaaattg catgaatagg ctctgctaac cgtgatgaga caaactgaaa 5220
attattgcaa gcattgacta taattatgca gtacgttctc aggatgcac caggggttca 5280
ttttcatgag cctgtccagg ttagtttact cctgaccact aatagcattg tcatttgggc 5340
tttctgttga atgaatcaac aaaccacaat acttcttggg accttttgta ctttatttga 5400
actatgagtc tttatatttt cctgatgatg gtggctgtaa tatgttgagt tcagtttact 5460
aaagggttta ctattatggt ttgaaggagg tctcatgacc tctcagaaaa ggtgcacctc 5520
cctgaaattg catatatgta tatagacatg cacacgtgtg catttgtttg tatacatata 5580
tttgtccttc gtatagcaag ttttttgctc atcagcagag agcaacagat gttttattga 5640
gtgaagcctt aaaaagcaca caccacacac agctaactgc caaaatacat tgaccgtagt 5700
agctgttcaa ctctagtagc ttagaaatac acgtatggtt aatgttcagt ccaacaaacc 5760
acacacagta aatgtttatt aatagtcacg gttcgtattt taggtgactg aaattgcaac 5820
agtgatcata atgaggtttg ttaaaatgat agctatatcc aaaatgtcta tatgtttatt 5880
tggacttttg aggttaaaga cagtcataata aacgtcctgt ttctgtttta atgttatcat 5940
agaatttttt aatgaaacta aattcaattg aaataaatga tagttttcat ctccaaaaaa 6000
aaaaaaaaag ggcgggccgc tcgagtctag agggcccggt ttaaaccgcg tgatcagcct 6060
cgactgtgcc ttctagtgtc cagccatctg ttgtttggcc ctcccccggt ccttccttga 6120
ccctggaagg ggccactccc
6140

```

<210> 537

<211> 1228

<212> PRT

<213> Homo sapiens

<400> 537

```

Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala
      5                      10                      15

```

```

Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
      20                      25                      30

```

```

Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
      35                      40                      45

```

```

Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
      50                      55                      60

```

```

Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu

```


65		70		75		80
Thr Arg Ala Ile	Ile Lys Cys Tyr Trp Lys	Ser Tyr Leu Val	Leu Gly			
	85	90	95			
Ile Phe Thr Leu	Ile Glu Glu Ser Ala Lys Val	Ile Gln Pro	Ile Phe			
	100	105	110			
Leu Gly Lys Ile	Ile Asn Tyr Phe Glu Asn Tyr Asp	Pro Met Asp	Ser			
	115	120	125			
Val Ala Leu Asn	Thr Ala Tyr Ala Tyr Ala Thr	Val Leu Thr	Phe Cys			
	130	135	140			
Thr Leu Ile Leu	Ala Ile Leu His His Leu Tyr Phe	Tyr His Val	Gln			
	145	150	155	160		
Cys Ala Gly Met	Arg Leu Arg Val Ala Met Cys His Met	Ile Tyr Arg				
	165	170	175			
Lys Ala Leu Arg	Leu Ser Asn Met Ala Met Gly Lys Thr	Thr Thr Gly				
	180	185	190			
Gln Ile Val Asn	Leu Leu Ser Asn Asp Val Asn Lys Phe	Asp Gln Val				
	195	200	205			
Thr Val Phe Leu	His Phe Leu Trp Ala Gly Pro Leu Gln	Ala Ile Ala				
	210	215	220			
Val Thr Ala Leu	Leu Trp Met Glu Ile Gly Ile Ser Cys	Leu Ala Gly				
	225	230	235	240		
Met Ala Val Leu	Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe	Gly Lys				
	245	250	255			
Leu Phe Ser Ser	Leu Arg Ser Lys Thr Ala Thr Phe Thr	Asp Ala Arg				
	260	265	270			
Ile Arg Thr Met	Asn Glu Val Ile Thr Gly Ile Arg Ile	Ile Lys Met				
	275	280	285			
Tyr Ala Trp Glu	Lys Ser Phe Ser Asn Leu Ile Thr Asn	Leu Arg Lys				
	290	295	300			
Lys Glu Ile Ser	Lys Ile Leu Arg Ser Ser Cys Leu Arg	Gly Met Asn				
	305	310	315	320		
Leu Ala Ser Phe	Phe Ser Ala Ser Lys Ile Ile Val Phe	Val Thr Phe				
	325	330	335			
Thr Thr Tyr Val	Leu Leu Gly Ser Val Ile Thr Ala Ser	Arg Val Phe				
	340	345	350			
Val Ala Val Thr	Leu Tyr Gly Ala Val Arg Leu Thr	Val Thr Leu Phe				
	355	360	365			
Phe Pro Ser Ala	Ile Glu Arg Val Ser Glu Ala Ile Val	Ser Ile Arg				
	370	375	380			

Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
 385 390 395 400
 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
 405 410 415
 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
 420 425 430
 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
 435 440 445
 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
 450 455 460
 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
 465 470 475 480
 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
 485 490 495
 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
 500 505 510
 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
 515 520 525
 Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
 530 535 540
 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
 545 550 555 560
 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
 565 570 575
 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
 580 585 590
 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
 595 600 605
 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
 610 615 620
 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
 625 630 635 640
 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
 645 650 655
 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
 660 665 670
 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
 675 680 685

Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
 690 695 700
 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
 705 710 715 720
 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
 725 730 735
 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
 740 745 750
 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr
 755 760 765
 Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu
 770 775 780
 Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys
 785 790 795 800
 Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn
 805 810 815
 Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu
 820 825 830
 Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu
 835 840 845
 Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile
 850 855 860
 Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg
 865 870 875 880
 Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr
 885 890 895
 Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp
 900 905 910
 Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp
 915 920 925
 Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr
 930 935 940
 Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val
 945 950 955 960
 Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala
 965 970 975
 Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met
 980 985 990
 Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile

Gln Lys Pro Ser Leu Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser
35 40 45

Tyr Leu Val Leu Gly Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val
 50 55 60
 Ile Gln Pro Ile Phe Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr
 65 70 75 80
 Asp Pro Met Asp Ser Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr
 85 90 95
 Val Leu Thr Phe Cys Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr
 100 105 110
 Phe Tyr His Val Gln Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys
 115 120 125
 His Met Ile Tyr Arg Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly
 130 135 140
 Lys Thr Thr Thr Gly Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn
 145 150 155 160
 Lys Phe Asp Gln Val Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro
 165 170 175
 Leu Gln Ala Ile Ala Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile
 180 185 190
 Ser Cys Leu Ala Gly Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln
 195 200 205
 Ser Cys Phe Gly Lys Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr
 210 215 220
 Phe Thr Asp Ala Arg Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile
 225 230 235 240
 Arg Ile Ile Lys Met Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile
 245 250 255
 Thr Asn Leu Arg Lys Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys
 260 265 270
 Leu Arg Gly Met Asn Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile
 275 280 285
 Val Phe Val Thr Phe Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr
 290 295 300
 Ala Ser Arg Val Phe Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu
 305 310 315 320
 Thr Val Thr Leu Phe Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala
 325 330 335
 Ile Val Ser Ile Arg Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile
 340 345 350

Ser Gln Arg Asn Arg Gln Leu Pro Ser Asp Gly Lys Lys Met Val His
 355 360 365
 Val Gln Asp Phe Thr Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr
 370 375 380
 Leu Gln Gly Leu Ser Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val
 385 390 395 400
 Val Gly Pro Val Gly Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu
 405 410 415
 Gly Glu Leu Ala Pro Ser His Gly Leu Val Ser Val His Gly Arg Ile
 420 425 430
 Ala Tyr Val Ser Gln Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser
 435 440 445
 Asn Ile Leu Phe Gly Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val
 450 455 460
 Ile Lys Ala Cys Ala Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly
 465 470 475 480
 Asp Leu Thr Val Ile Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln
 485 490 495
 Lys Ala Arg Val Asn Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile
 500 505 510
 Tyr Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg
 515 520 525
 His Leu Phe Glu Leu Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr
 530 535 540
 Ile Leu Val Thr His Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile
 545 550 555 560
 Leu Ile Leu Lys Asp Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu
 565 570 575
 Phe Leu Lys Ser Gly Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn
 580 585 590
 Glu Glu Ser Glu Gln Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn
 595 600 605
 Arg Thr Phe Ser Glu Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro
 610 615 620
 Ser Leu Lys Asp Gly Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro
 625 630 635 640
 Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln
 645 650 655
 Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile

660					665					670						
Phe	Leu	Ile	Leu	Leu	Asn	Thr	Ala	Ala	Gln	Val	Ala	Tyr	Val	Leu	Gln	
675					680					685						
Asp	Trp	Trp	Leu	Ser	Tyr	Trp	Ala	Asn	Lys	Gln	Ser	Met	Leu	Asn	Val	
690					695					700						
Thr	Val	Asn	Gly	Gly	Gly	Asn	Val	Thr	Glu	Lys	Leu	Asp	Leu	Asn	Trp	
705					710					715					720	
Tyr	Leu	Gly	Ile	Tyr	Ser	Gly	Leu	Thr	Val	Ala	Thr	Val	Leu	Phe	Gly	
725					730					735						
Ile	Ala	Arg	Ser	Leu	Leu	Val	Phe	Tyr	Val	Leu	Val	Asn	Ser	Ser	Gln	
740					745					750						
Thr	Leu	His	Asn	Lys	Met	Phe	Glu	Ser	Ile	Leu	Lys	Ala	Pro	Val	Leu	
755					760					765						
Phe	Phe	Asp	Arg	Asn	Pro	Ile	Gly	Arg	Ile	Leu	Asn	Arg	Phe	Ser	Lys	
770					775					780						
Asp	Ile	Gly	His	Leu	Asp	Asp	Leu	Leu	Pro	Leu	Thr	Phe	Leu	Asp	Phe	
785					790					795					800	
Ile	Gln	Thr	Leu	Leu	Gln	Val	Val	Gly	Val	Val	Ser	Val	Ala	Val	Ala	
805					810					815						
Val	Ile	Pro	Trp	Ile	Ala	Ile	Pro	Leu	Val	Pro	Leu	Gly	Ile	Ile	Phe	
820					825					830						
Ile	Phe	Leu	Arg	Arg	Tyr	Phe	Leu	Glu	Thr	Ser	Arg	Asp	Val	Lys	Arg	
835					840					845						
Leu	Glu	Ser	Thr	Thr	Arg	Ser	Pro	Val	Phe	Ser	His	Leu	Ser	Ser	Ser	
850					855					860						
Leu	Gln	Gly	Leu	Trp	Thr	Ile	Arg	Ala	Tyr	Lys	Ala	Glu	Glu	Arg	Cys	
865					870					875					880	
Gln	Glu	Leu	Phe	Asp	Ala	His	Gln	Asp	Leu	His	Ser	Glu	Ala	Trp	Phe	
885					890					895						
Leu	Phe	Leu	Thr	Thr	Ser	Arg	Trp	Phe	Ala	Val	Arg	Leu	Asp	Ala	Ile	
900					905					910						
Cys	Ala	Met	Phe	Val	Ile	Ile	Val	Ala	Phe	Gly	Ser	Leu	Ile	Leu	Ala	
915					920					925						
Lys	Thr	Leu	Asp	Ala	Gly	Gln	Val	Gly	Leu	Ala	Leu	Ser	Tyr	Ala	Leu	
930					935					940						
Thr	Leu	Met	Gly	Met	Phe	Gln	Trp	Cys	Val	Arg	Gln	Ser	Ala	Glu	Val	
945					950					955					960	
Glu	Asn	Met	Met	Ile	Ser	Val	Glu	Arg	Val	Ile	Glu	Tyr	Thr	Asp	Leu	
965					970					975						

Glu Lys Glu Ala Pro Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp
 980 985 990
 Pro His Glu Gly Val Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser
 995 1000 1005
 Pro Gly Gly Pro Leu Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser
 1010 1015 1020
 Gln Glu Lys Val Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser
 1025 1030 1035 1040
 Leu Ile Ser Ala Leu Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp
 1045 1050 1055
 Ile Asp Lys Ile Leu Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys
 1060 1065 1070
 Lys Met Ser Ile Ile Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met
 1075 1080 1085
 Arg Lys Asn Leu Asp Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp
 1090 1095 1100
 Asn Ala Leu Gln Glu Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro
 1105 1110 1115 1120
 Gly Lys Met Asp Thr Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val
 1125 1130 1135
 Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn
 1140 1145 1150
 Gln Ile Leu Ile Ile Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr
 1155 1160 1165
 Asp Glu Leu Ile Gln Lys Lys Ile Arg Glu Lys Phe Ala His Cys Thr
 1170 1175 1180
 Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys
 1185 1190 1195 1200
 Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr
 1205 1210 1215
 Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln
 1220 1225 1230
 Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg
 1235 1240 1245
 Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser
 1250 1255 1260

<210> 539

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 539

Cys Leu Ser His Ser Val Ala Val Val Thr
1 5 10

<210> 540

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 540

Ala Val Val Thr Ala Ser Ala Ala Leu
1 5

<210> 541

<211> 14

<212> PRT

<213> Homo sapiens

<400> 541

Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu
5 10

<210> 542

<211> 15

<212> PRT

<213> Homo sapiens

<400> 542

Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala
5 10 15

<210> 543

<211> 12

<212> PRT

<213> Homo sapiens

<400> 543

Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val
5 10

<210> 544

<211> 18

<212> PRT

<213> Homo sapiens

<400> 544

Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe

5

10

15

Met Thr

<210> 545

<211> 18

<212> PRT

<213> Homo sapiens

<400> 545

Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
5 10 15

Ser Val

<210> 546

<211> 29

<212> PRT

<213> Homo sapiens

<400> 546

Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly
5 10 15

Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met
20 25

<210> 547

<211> 58

<212> PRT

<213> Homo sapiens

<400> 547

Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu
5 10 15

Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu
20 25 30

Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys
35 40 45

Cys Arg Met Pro Arg Thr Leu Arg Arg Leu
50 55

<210> 548

<211> 18

<212> PRT

<213> Homo sapiens

<400> 548

Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu

200

5

10

15

Glu Cys

<210> 549

<211> 18

<212> PRT

<213> Homo sapiens

<400> 549

Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg

5

10

15

Gln Ala

<210> 550

<211> 14

<212> PRT

<213> Homo sapiens

<400> 550

Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe

5

10

<210> 551

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 551

Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala

1

5

10

THIS PAGE BLANK (USPTO)